

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 2, 2006, 12:47:32 ; Search time 61 Seconds  
(without alignments)  
1476.601 Million cell updates/sec

Title: US-10-087-190-3  
Perfect score: 1047  
Sequence: 1 MSKKKGLSAEKRTTRMEIF.....FEENKIDRTFGIPDPDYID 205

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21:.\*  
1: Geneseqp1980s:.\*  
2: Geneseqp1990s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004s:.\*  
9: Geneseqp2005s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1047	100.0	205	7	ADD84537
2	1047	100.0	205	7	ADJ70015 Human hea
3	1047	100.0	205	8	ADM83851 Human can
4	1047	100.0	205	8	ADM83810 Human can
5	1047	100.0	205	8	ADM83812 Human can
6	1047	100.0	205	8	ADM83793 Human can
7	1047	100.0	205	8	ADM83811 Human can
8	1047	100.0	205	8	ADM83804 Human can
9	1047	100.0	219	6	ABP75541 Human sec
10	1036.5	99.0	206	8	ADM83834 Human can
11	1036.5	99.0	206	8	ADM83835 Human can
12	1011	96.6	198	8	ADM83814 Human can
13	975	93.1	190	4	AAM40043 Human pol
14	975	93.1	190	7	ADD84547 Human pol
15	975	93.1	190	8	ADM83857 Human can
16	975	93.1	190	8	ADM83859 Human can
17	975	93.1	190	8	ADM83803 Human can
18	975	93.1	190	8	ADM83809 Human can
19	975	93.1	190	8	ADM83858 Human can
20	948	90.5	205	8	ADM83813 Mouse hyp
21	945.5	90.3	190	7	ADD84545 Human can
22	945.5	90.3	190	8	ADM83808 Human can
23	945.5	90.3	190	8	ADM83801 Human can
24	945.5	90.3	190	8	ADM83853 Human can

25	945.5	90.3	190	8	ADM83852 Human can
26	614	58.6	122	4	ADM83843 Human can
27	606	57.9	122	4	AAM41829 Human pol
28	591	56.4	122	7	ADD84543 Human can
29	591	56.4	122	8	ADM83799 Human can
30	591	56.4	122	8	ADM83845 Human can
31	591	56.4	122	8	ADM83807 Human can
32	591	56.4	122	8	ADM83844 Human can
33	584	55.8	119	7	ADD84541 Human can
34	584	55.8	119	8	ADM83797 Human can
35	584	55.8	119	8	ADM83806 Human can
36	584	55.8	119	8	ADM83837 Human can
37	465	44.4	126	7	ADD84539 Human can
38	465	44.4	126	8	ADM83836 Human can
39	465	44.4	126	8	ADM83795 Human can
40	465	44.4	126	8	ADM83805 Human can
41	349	33.3	200	8	ADM83815 Human can
42	329.5	31.5	182	4	ABG12341 Novel hum
43	287	27.4	79	4	AAg74669 Yeast SMO
44	255.5	24.4	218	5	ADH32846 Yeast SMO
45	135.5	12.9	1281	8	ADP26646 Mouse dyn

## ALIGNMENTS

RESULT 1  
ADD84537  
ID ADD84537 standard; protein; 205 AA.  
XX  
AC ADD84537;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE 121P1FI protein.  
XX  
KW 121P1FI; 121P1FI modulation; human; chromosome 4q; cytostatic;  
KW gene therapy; vaccine; cancer; immune response; immunisation.  
XX  
OS Homo sapiens.  
XX  
FN WO200295009-A2.  
XX  
PD 28-NOV-2002.  
XX  
PF 28-FEB-2002; 2002MO-US006242.  
XX  
PR 05-MAR-2001; 2001US-00799250.  
XX  
PA (AGEN-) AGENSYS INC.  
XX  
PI Chailita-Bid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W;  
PI Jakobovits A;  
XX  
DR WPI; 2003-156757/15.  
XX  
N-PsDB; ADD84536.  
XX  
PT Composition comprising a substance that modulates the status of 121P1FI,  
PT useful in diagnosing, preventing, prognosticating or treating patients  
PT with cancer that expresses 121P1FI, such as breast, colon, ovarian or  
PT lung cancer.  
XX  
PS Claim 19; Fig 2A; 285pp; English.  
XX  
CC The present invention describes a composition (I) comprising a substance  
CC that modulates the status of 121P1FI (gene and encoded protein), or a  
CC molecule that is modulated by 121P1FI, where the status of a cell that  
CC expresses 121P1FI is modulated. The human 121P1FI gene maps to chromosome  
CC 4q (I) has cytostatic activity, and can be used in gene therapy, and in  
CC vaccines. The composition (I) can be used for diagnosing, preventing,  
CC prognosticating or treating patients with cancer that expresses 121P1FI,  
CC such as breast, colon, ovarian or lung cancer. The 121P1FI gene or its  
CC fragment can be used to elicit a humoral or cellular immune response.

CC 121P1F1 antibodies can be used in active or passive immunisation. 121P1F1  
 CC polynucleotides are useful as probes and primers for the amplification or  
 CC detection of 121P1F1 genes, as coding sequences for directing the  
 CC expression of 121P1F1 polypeptides, or as tools for modulating or  
 CC inhibiting the expression of 121P1F1 genes. The present sequence is used  
 CC in the exemplification of the present invention.

XX Sequence 205 AA;

Query Match 100.0%; Score 1047; DB 7; Length 205;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-88;  
 Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSKKKGSAEKKRTRMMEIFSETDVPOLKLEKIAPEKIGITMSYKEVLQSLVDDGMV 60

Db 1 MSKKKGSAEKKRTRMMEIFSETDVPOLKLEKIAPEKIGITMSYKEVLQSLVDDGMV 60

Qy 61 DCEIRIGTSNYMAPPSPKALHARKHLEVLSEQLSEGSQKHAISLOKSIKAKIGRCETEE 120

Db 61 DCEIRIGTSNYMAPPSPKALHARKHLEVLSEQLSEGSQKHAISLOKSIKAKIGRCETEE 120

Qy 121 TRLAKELSLRDQREQLKAEVEKYKCDPQVVEEIRQANKYAKAANRMTDNIFAISMA 180

Db 121 TRLAKELSLRDQREQLKAEVEKYKCDPQVVEEIRQANKYAKAANRMTDNIFAISMA 180

Qy 181 KRKGFEEENKIDRTFGIPEDFDYID 205

Db 181 KRKGFEEENKIDRTFGIPEDFDYID 205

RESULT 2

ADJ70015 ADJ70015 standard; protein; 205 AA.

XX ADJ70015;

XX 06-MAY-2004 (first entry)

XX Human heat mitochondrial protein as a therapeutic target SegID1821.

XX mitochondrial; human; screening assay; diabetes mellitus;

XX Huntington's disease; osteoarthritis;

XX Leber's hereditary optic neuropathy; LHON;

XX mitochondrial encephalopathy lactic acidosis and stroke; MELAS;

XX myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;

XX neuroprotective; nocrotropic; antidiabetic; anticonvulsant; antiarthritic;

XX osteopathic; ophthalmological; cytosstatic.

XX Homo sapiens.

XX WO2003087768-A2.

XX 23-OCT-2003.

XX 04-APR-2003; 2003WO-US010870.

XX 12-APR-2002; 2002US-0372843P.

XX 17-JUN-2002; 2002US-038987P.

XX 20-SEP-2002; 2002US-0412418P.

XX (MITO-) MITOKOR.

XX (BUCK-) BUCK INST AGE RES.

XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GW,  
 XX Warnock DE;

XX WPI; 2003-845369/78.

XX Identifying a mitochondrial target for drug screening assays and for  
 XX treating diseases associated with altered mitochondrial function,  
 XX comprises detecting a modified polypeptide in a sample and correlating  
 XX with the disease.

PS Claim 1; SEQ ID NO 1821; 180pp; English.

XX This invention relates to novel mitochondrial targets that can be used  
 CC for therapeutic intervention in treating a disease associated with  
 CC altered mitochondrial function. Specifically, it refers to a method for  
 CC identifying proteins of the human heart mitochondrial proteome that are  
 CC useful for drug screening assays, as well as therapeutic targets. The  
 CC present invention describes a method for identifying such proteins that  
 CC can be used in the treatment of various diseases associated with altered  
 CC mitochondrial function including diabetes mellitus, Huntington's disease,  
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial  
 CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy  
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these  
 CC compositions have neuroprotective, nocrotropic, antidiabetic,  
 CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and  
 CC cytosstatic activities. This polypeptide sequence is a human heart  
 CC mitochondrial protein of the invention.

XX Sequence 205 AA;

Query Match 100.0%; Score 1047; DB 7; Length 205;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-88;  
 Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSKKKGSAEKKRTRMMEIFSETDVPOLKLEKIAPEKIGITMSYKEVLQSLVDDGMV 60

Db 1 MSKKKGSAEKKRTRMMEIFSETDVPOLKLEKIAPEKIGITMSYKEVLQSLVDDGMV 60

Qy 61 DCEIRIGTSNYMAPPSPKALHARKHLEVLSEQLSEGSQKHAISLOKSIKAKIGRCETEE 120

Db 61 DCEIRIGTSNYMAPPSPKALHARKHLEVLSEQLSEGSQKHAISLOKSIKAKIGRCETEE 120

Qy 121 TRLAKELSLRDQREQLKAEVEKYKCDPQVVEEIRQANKYAKAANRMTDNIFAISMA 180

Db 121 TRLAKELSLRDQREQLKAEVEKYKCDPQVVEEIRQANKYAKAANRMTDNIFAISMA 180

Qy 181 KRKGFEEENKIDRTFGIPEDFDYID 205

Db 181 KRKGFEEENKIDRTFGIPEDFDYID 205

RESULT 3

ADM83851 ADM83851 standard; protein; 205 AA.

XX ADM83851;

XX 03-JUN-2004 (first entry)

XX Human cancer gene 121P1F1 protein #6.

XX Human cancer gene 121P1F1; cytosstatic; cancer; chromosome 4q; HLA;

XX human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;

XX colon cancer; lung cancer; pancreatic cancer; breast cancer;

XX cervical cancer; stomach cancer; gene therapy; vaccine.

XX Homo sapiens.

XX US2003223997-A1.

XX 04-DEC-2003.

XX 28-FEB-2002; 2002US-00087190.

XX 08-FEB-2001; 2001US-00779250.

XX (CHAL/) CHALLITA-EID P M.

XX (HUBB/) HUBERT R S.

XX (RAIT/) RAITANO A B.

XX (APAR/) APAR D E H.

XX (GERW/) GE W.

XX (JAKO/) JAKOBOVITS A.

```

XX  Chailite-Bld PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W,
PI  Jakobovits A;
XX  WPI, 2004-060522/06.
DR
XX
XX  New composition comprising a substance that modulates the status of
PT  121PI1 or a molecule that is modulated by 121PI1, useful for detecting,
PT  treating or preventing cancer e.g. prostate, bladder, colon, breast or
PT  lung cancer.
PS
XX  Example 5; SEQ ID NO 61; 211pp; English.
XX
XX  The invention relates to a composition comprising a substance that
CC  modulates the status of 121PI1 (a protein encoded by a cancer expressed
CC  gene) or a molecule that is modulated by 121PI1 where status of the cell
CC  that expresses 121PI1 is modulated. Also included are a pharmaceutical
CC  composition comprising the novel composition in a human unit dose form, a
CC  recombinant protein comprising an antigen-binding region of a monoclonal
CC  antibody, a non-human transgenic animal that produces an antibody, a
CC  hydridoma that produces an antibody, a single chain monoclonal antibody
CC  that immunospecifically binds to a 121PI1-related protein (comprising
CC  the variable domains of the heavy and light chains of a monoclonal
CC  antibody), a vector comprising a polynucleotide that encodes a single
CC  chain monoclonal antibody, a polynucleotide that encodes an analogue
CC  peptide, delivering a cytotoxic agent or a diagnostic agent to a cell
CC  that expresses 121PI1, inhibiting growth of cancer cells that expresses
CC  121PI1 (comprising administering to the cells the composition), treating
CC  a patient who bears cancer cells that express 121PI1, generating a
CC  mammalian immune response directed to 121PI1, inducing an immune
CC  response, monitoring 121PI1 gene products in a biological sample from a
CC  patient who has or who is suspected of having cancer, monitoring the
CC  presence of cancer in an individual and an assay for detecting the
CC  presence of a 121PI1-related protein or polynucleotide in a biological
CC  sample from a patient who has or who is suspected of having cancer. The
CC  composition may comprise a polynucleotide that comprises a 121PI1-
CC  related protein coding sequence provided that the coding sequence does
CC  not encode the entire amino acid sequence of 121PI1 (ADMB3793). The
CC  substance also comprises a polynucleotide that encodes at least one
CC  peptide given in 16 Tables (given in the specification), the peptides
CC  being HLA (human leukocyte antigen)-binding epitopes from 121PI1 or its
CC  splice variants. The composition is useful for detecting, treating or
CC  preventing cancer, preferably prostate cancer, bladder cancer, kidney
CC  cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer,
CC  cervical cancer or stomach cancer. The composition can also be used as a
CC  vaccine to treat or prevent cancer that expresses or overexpresses
CC  121PI1. The gene for 121PI1 is located on chromosome 4q. The present
CC  sequence is a 121PI1 protein (full-length or fragment).
XX
XX  Sequence 205 AA;
SQ
XX
XX  Query Match 100.0%; Score 1047; DB 8; Length 205;
XX  Best Local Similarity 100.0%; Pred. No. 1.8e-88;
XX  Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
QY  1 MSKKKGLSNEKRTMMEIFSEKTVFQKDXDEKIAPKKGGITANSVKVEVLSLVDDGVY 60
Db  1 MSKKKGLSNEKRTMMEIFSEKTVFQKDXDEKIAPKKGGITANSVKVEVLSLVDDGVY 60
QY  61 DCEKIGTSNYWYAFPSKALHARKHKLVEVLSQSESSQYHSLQNSIEKAKTGRCTEER 120
Db  61 DCEKIGTSNYWYAFPSKALHARKHKLVEVLSQSESSQYHSLQNSIEKAKTGRCTEER 120
QY  121 TRLAEKLSLRQROQLKAVEKYKDDQCVYVEIRQAKNVKAEANRMTDNIFAIKSMA 180
Db  121 TRLAEKLSLRQROQLKAVEKYKDDQCVYVEIRQAKNVKAEANRMTDNIFAIKSMA 180
QY  181 KRKFGFEENKIDRTFGIIPEDFYID 205
Db  181 KRKFGFEENKIDRTFGIIPEDFYID 205

```

AD	ADM83810	standard; protein; 205 AA.
ID	ADM83810	standard; protein; 205 AA.
AC	ADM83810;	
XX		
DT	03-JUN-2004	(first entry)
XX		
DE	Human cancer gene 121P1F1 protein #3.	
XX		
KW	Human; cancer gene 121P1F1; cytosolic; cancer; chromosome 4q; HLA;	
KW	human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;	
KW	colon cancer; lung cancer; pancreatic cancer; breast cancer;	
KW	cervical cancer; stomach cancer; gene therapy; vaccine.	
OS	Homo sapiens.	
XX		
PN	US2003223997-A1.	
XX		
PD	04-DEC-2003.	
XX		
PF	28-FEB-2002; 2002US-00087190.	
XX		
PR	08-FEB-2001; 2001US-00779250.	
XX		
PA	(CHAL/) CHALLITA-BID P M.	
PA	(HUBE/) HUBERT R S.	
PA	(RAIT/) RAITANO A B.	
PA	(FARI/) FARIS M.	
PA	(AFAR/) AFAR D E H.	
PA	(GEWU/) GE W.	
PA	(JAKO/) JAKOBOVITS A.	
XX		
PI	Challita-Bid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W;	
PI	Jakovovits A;	
XX		
DR	WPI: 2004-060522/06.	
XX		
PT	New composition comprising a substance that modulates the status of	
PT	121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting,	
PT	treating or preventing cancer e.g. prostate, bladder, colon, breast or	
PT	lung cancer.	
XX		
XX		
PS	Disclosure; SEQ ID NO 20; 21bp; English.	
XX		
CC	The invention relates to a composition comprising a substance that	
CC	modulates the status of 121P1F1 (a protein encoded by a cancer expressed	
CC	gene) or a molecule that is modulated by 121P1F1 where status of the cell	
CC	that expresses 121P1F1 is modulated. Also included are a pharmaceutical	
CC	composition comprising the novel composition in a human unit dose form, a	
CC	recombinant protein comprising an antigen-binding region of a monoclonal	
CC	antibody, a non-human transgenic animal that produces an antibody, a	
CC	hybridoma that produces an antibody, a single chain monoclonal antibody	
CC	that immunospecifically binds to a 121P1F1-related protein (comprising	
CC	the variable domains of the heavy and light chains of a monoclonal	
CC	antibody), a vector comprising a polynucleotide that encodes a single	
CC	chain monoclonal antibody, a polynucleotide that encodes an analogue	
CC	peptide, delivering a cytotoxic agent or a diagnostic agent to a cell	
CC	that expresses 121P1F1, inhibiting growth of cancer cells that expresses	
CC	121P1F1 (comprising administering to the cells the composition), treating	
CC	a patient who bears cancer cells that express 121P1F1, generating a	
CC	mammalian immune response directed to 121P1F1, inducing an immune	
CC	response, monitoring 121P1F1 gene products in a biological sample from a	
CC	patient who has or who is suspected of having cancer, monitoring the	
CC	presence of cancer in an individual and an assay for detecting the	
CC	presence of a 121P1F1-related protein or polynucleotide in a biological	
CC	sample from a patient who has or who is suspected of having cancer. The	
CC	composition may comprise a polynucleotide that comprises a 121P1F1-	
CC	related protein coding sequence provided that the coding sequence does	
CC	not encode the entire amino acid sequence of 121P1F1 (ADM83793). The	
CC	substance also comprises a polynucleotide that encodes at least one	
CC	peptide given in 16 Tables (given in the specification), the peptides	
CC	being HLA (human leukocyte antigen)-binding epitopes from 121P1F1 or its	
CC	splice variants. The composition is useful for detecting, treating or	

CC preventing cancer, preferably prostate cancer, bladder cancer, kidney  
CC cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer,  
CC cervical cancer or stomach cancer. The composition can also be used as a  
CC vaccine to treat or prevent cancer that expresses or overexpresses  
CC 121PI1. The gene for 121PI1 is located on chromosome 4q. The present  
CC sequence is a 121PI1 protein (full-length or fragment).  
XX  
SQ Sequence 205 AA;  
Query Match 100.0%; Score 1047; DB 8; Length 205;  
Best Local Similarity 100.0%; Pred. No. 1.8e-88;  
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MSKKKGSAEKKRTMMEIFSETQVFLQKDLKIAPEKIGITAMSYKVLQSLVDDGMV 60  
DB 1 MSKKKGSAEKKRTMMEIFSETQVFLQKDLKIAPEKIGITAMSYKVLQSLVDDGMV 60  
QY 61 DCEKIGTNTYMAFPSPKALHARKHKLTVLSQLSBGSQKASLQKSIKAKIGRCETTER 120  
DB 61 DCEKIGTNTYMAFPSPKALHARKHKLTVLSQLSBGSQKASLQKSIKAKIGRCETTER 120  
QY 121 TRLAKELSLRDQREOLKAVEKYKDCDPQVVEIRQANKYAKAARMTDNIPIKSWA 180  
DB 121 TRLAKELSLRDQREOLKAVEKYKDCDPQVVEIRQANKYAKAARMTDNIPIKSWA 180  
QY 181 KRKGFEEKNIDRTFGIPEDFDYID 205  
DB 181 KRKGFEEKNIDRTFGIPEDFDYID 205  
RESULT 5  
ADM83812  
ID ADM83812 standard; protein; 205 AA.  
XX  
AC ADM83812;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE Human cancer gene 121PI1 protein #5.  
XX  
XX Human; cancer gene 121PI1; cytostatic; cancer; chromosome 4q; HLA;  
KM human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;  
KM colon cancer; lung cancer; pancreatic cancer; breast cancer;  
KM cervical cancer; stomach cancer; gene therapy; vaccine.  
XX  
OS Homo sapiens.  
XX  
PN US2003223997-A1.  
XX  
PD 04-DEC-2003.  
XX  
PF 28-FEB-2002; 2002US-00087190.  
XX  
PR 08-FEB-2001; 2001US-00779250.  
XX  
PA (CHAL/) CHALLITA-EID P M.  
PA (HUBE/) HUBERT R S.  
PA (RAIT/) RAITANO A B.  
PA (FARI/) FARIS M.  
PA (AFAR/) AFAR D E H.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
XX  
PI Challita-Eid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W;  
PI Jakobovits A;  
XX  
DR WPI; 2004-060522/06.  
XX  
PT New composition comprising a substance that modulates the status of  
PT 121PI1 or a molecule that is modulated by 121PI1, useful for detecting,  
PT treating or preventing cancer e.g. prostate, bladder, colon, breast or  
XX lung cancer.  
XX

PS Disclosure; SEQ ID NO 22; 211pp; English.  
XX  
XX The invention relates to a composition comprising a substance that  
CC modules the status of 121PI1 (a protein encoded by a cancer expressed  
CC gene) or a molecule that is modulated by 121PI1 where status of the cell  
CC that expresses 121PI1 is modulated. Also included are a pharmaceutical  
CC composition comprising the novel composition in a human unit dose form, a  
CC recombinant protein comprising an antigen-binding region of a monoclonal  
CC antibody, a non-human transgenic animal that produces an antibody, a  
CC hybridoma that produces an antibody, a single chain monoclonal antibody  
CC that immunospecifically binds to a 121PI1-related protein (comprising  
CC the variable domains of the heavy and light chains of a monoclonal  
CC antibody), a vector comprising a polynucleotide that encodes a single  
CC chain monoclonal antibody, a polynucleotide that encodes an analogue  
CC peptide, delivering a cytotoxic agent or a diagnostic agent to a cell  
CC that expresses 121PI1, inhibiting growth of cancer cells that expresses  
CC 121PI1 (comprising administering to the cells the composition), treating  
CC a patient who bears cancer cells that express 121PI1, generating a  
CC mammalian immune response directed to 121PI1, inducing an immune  
CC response, monitoring 121PI1 gene products in a biological sample from a  
CC patient who has or who is suspected of having cancer, monitoring the  
CC presence of cancer in an individual and an assay for detecting the  
CC presence of a 121PI1-related protein or polynucleotide in a biological  
CC sample from a patient who has or who is suspected of having cancer. The  
CC composition may comprise a polynucleotide that comprises a 121PI1-  
CC related protein coding sequence provided that the coding sequence does  
CC not encode the entire amino acid sequence of 121PI1 (ADM83793). The  
CC substance also comprises a polynucleotide that encodes at least one  
CC peptide given in 16 Tables (given in the specification), the peptides  
CC being HLA (human leukocyte antigen)-binding epitopes from 121PI1 or its  
CC splice variants. The composition is useful for detecting, treating or  
CC preventing cancer, preferably prostate cancer, bladder cancer, kidney  
CC cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer,  
CC cervical cancer or stomach cancer. The composition can also be used as a  
CC vaccine to treat or prevent cancer that expresses or overexpresses  
CC 121PI1. The gene for 121PI1 is located on chromosome 4q. The present  
CC sequence is a 121PI1 protein (full-length or fragment).  
XX  
SQ Sequence 205 AA;  
Query Match 100.0%; Score 1047; DB 8; Length 205;  
Best Local Similarity 100.0%; Pred. No. 1.8e-88;  
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MSKKKGSAEKKRTMMEIFSETQVFLQKDLKIAPEKIGITAMSYKVLQSLVDDGMV 60  
DB 1 MSKKKGSAEKKRTMMEIFSETQVFLQKDLKIAPEKIGITAMSYKVLQSLVDDGMV 60  
QY 61 DCEKIGTNTYMAFPSPKALHARKHKLTVLSQLSBGSQKASLQKSIKAKIGRCETTER 120  
DB 61 DCEKIGTNTYMAFPSPKALHARKHKLTVLSQLSBGSQKASLQKSIKAKIGRCETTER 120  
QY 121 TRLAKELSLRDQREOLKAVEKYKDCDPQVVEIRQANKYAKAARMTDNIPIKSWA 180  
DB 121 TRLAKELSLRDQREOLKAVEKYKDCDPQVVEIRQANKYAKAARMTDNIPIKSWA 180  
QY 181 KRKGFEEKNIDRTFGIPEDFDYID 205  
DB 181 KRKGFEEKNIDRTFGIPEDFDYID 205  
RESULT 6  
ADM83793  
ID ADM83793 standard; protein; 205 AA.  
XX  
AC ADM83793;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE Human cancer gene 121PI1 protein #1.  
XX  
KM Human; cancer gene 121PI1; cytostatic; cancer; chromosome 4q; HLA;  
KM human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;  
XX

KM colon cancer; lung cancer; pancreatic cancer; breast cancer;  
 KM cervical cancer; stomach cancer; gene therapy; vaccine.  
 XX Homo sapiens.  
 XX US2003223997-A1.  
 XX  
 PD 04-DEC-2003.  
 XX  
 PF 28-FEB-2002; 2002US-00087190.  
 PR 08-FEB-2001; 2001US-00779250.  
 XX  
 PA (CHAL/) CHALLITA-EID P M.  
 PA (HUBE/) HUBERT R S.  
 PA (RAIT/) RAITANO A B.  
 PA (FARI/) FARIS M.  
 PA (AFAR/) AFAR D E H.  
 PA (GEW/) GE W.  
 PA (JAKO/) JAKOBOVITS A.  
 XX  
 PI Challita-Eid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W;  
 PI Jakobovits A;  
 XX  
 DR WPI; 2004-060522/06.  
 DR N-PSDB; ADM83792.  
 XX  
 PT New composition comprising a substance that modulates the status of  
 PT 121PIPI or a molecule that is modulated by 121PIPI, useful for detecting,  
 PT treating or preventing cancer e.g. prostate, bladder, colon, breast or  
 PT lung cancer.  
 XX  
 PS Claim 19; SEQ ID NO 3; 211pp; English.  
 XX  
 CC The invention relates to a composition comprising a substance that  
 CC modulates the status of 121PIPI (a protein encoded by a cancer expressed  
 CC gene) or a molecule that is modulated by 121PIPI where status of the cell  
 CC that expresses 121PIPI is modulated. Also included are a pharmaceutical  
 CC composition comprising the novel composition in a human unit dose form, a  
 CC recombinant protein comprising an antigen-binding region of a monoclonal  
 CC antibody, a non-human transgenic animal that produces an antibody, a  
 CC hybridoma that produces an antibody, a single chain monoclonal antibody  
 CC that immunospecifically binds to a 121PIPI-related protein (comprising  
 CC the variable domains of the heavy and light chains of a monoclonal  
 CC antibody), a vector comprising a polynucleotide that encodes a single  
 CC chain monoclonal antibody, a polynucleotide that encodes an analogue  
 CC peptide, delivering a cytotoxic agent or a diagnostic agent to a cell  
 CC that expresses 121PIPI, inhibiting growth of cancer cells that expresses  
 CC 121PIPI (comprising administering to the cells the composition), treating  
 CC a patient who bears cancer cells that express 121PIPI, generating a  
 CC mammalian immune response directed to 121PIPI, inducing an immune  
 CC response, monitoring 121PIPI gene products in a biological sample from a  
 CC patient who has or who is suspected of having cancer, monitoring the  
 CC presence of cancer in an individual and an assay for detecting the  
 CC presence of a 121PIPI-related protein or polynucleotide in a biological  
 CC sample from a patient who has or who is suspected of having cancer. The  
 CC composition may comprise a polynucleotide that comprises a 121PIPI-  
 CC related protein coding sequence provided that the coding sequence does  
 CC not encode the entire amino acid sequence of 121PIPI (ADM83793). The  
 CC substance also comprises a polynucleotide that encodes at least one  
 CC peptide given in 16 Tables (given in the specification), the peptides  
 CC being HLA (human leukocyte antigen)-binding epitopes from 121PIPI or its  
 CC splice variants. The composition is useful for detecting, treating or  
 CC preventing cancer, preferably prostate cancer, bladder cancer, kidney  
 CC cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer,  
 CC cervical cancer or stomach cancer. The composition can also be used as a  
 CC vaccine to treat or prevent cancer that expresses or overexpresses  
 CC 121PIPI. The gene for 121PIPI is located on chromosome 4q. The present  
 CC sequence is a 121PIPI protein (full-length or fragment).  
 XX  
 SQ Sequence 205 AA;  
 Query Match 100.0%; Score 1047; DB 8; Length 205;

Best Local Similarity 100.0%; Pred. No. 1.8e-88;  
 Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSKKKGLSAEKRRTMEI FSETKDV FOLKLEKIA PKKGTAMS VYKVLQSLVDGNY 60  
 DB 1 MSKKKGLSAEKRRTMEI FSETKDV FOLKLEKIA PKKGTAMS VYKVLQSLVDGNY 60  
 QY 61 DCEKIGTSNYWAPPSKALHARKHLEVLSEQLSGSQKHSLOKSIKAKTGRCTEER 120  
 DB 61 DCEKIGTSNYWAPPSKALHARKHLEVLSEQLSGSQKHSLOKSIKAKTGRCTEER 120  
 QY 121 TRLAKEISLADQREQLKAEVEKYKDCDPVVEEIRQANKYAKKANRWTDNI FAKSKMA 180  
 DB 121 TRLAKEISLADQREQLKAEVEKYKDCDPVVEEIRQANKYAKKANRWTDNI FAKSKMA 180  
 QY 181 KRKFGFEENKIDRTGPIPEDFDYID 205  
 DB 181 KRKFGFEENKIDRTGPIPEDFDYID 205  
 RESULT 7  
 ID ADM83811 standard; protein; 205 AA.  
 XX  
 AC ADM83811;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Human cancer gene 121PIPI protein #4.  
 XX  
 KW Human; cancer gene 121PIPI; cytostatic; cancer; chromosome 4q; HLA;  
 KW human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;  
 KW colon cancer; lung cancer; pancreatic cancer; breast cancer;  
 KW cervical cancer; stomach cancer; gene therapy; vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 US2003223997-A1.  
 XX  
 PD 04-DEC-2003.  
 XX  
 PF 28-FEB-2002; 2002US-00087190.  
 PR 08-FEB-2001; 2001US-00779250.  
 XX  
 PA (CHAL/) CHALLITA-EID P M.  
 PA (HUBE/) HUBERT R S.  
 PA (RAIT/) RAITANO A B.  
 PA (FARI/) FARIS M.  
 PA (AFAR/) AFAR D E H.  
 PA (GEW/) GE W.  
 PA (JAKO/) JAKOBOVITS A.  
 XX  
 PI Challita-Eid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W;  
 PI Jakobovits A;  
 XX  
 DR WPI; 2004-060522/06.  
 XX  
 PT New composition comprising a substance that modulates the status of  
 PT 121PIPI or a molecule that is modulated by 121PIPI, useful for detecting,  
 PT treating or preventing cancer e.g. prostate, bladder, colon, breast or  
 PT lung cancer.  
 XX  
 PS Disclosure; SEQ ID NO 21; 211pp; English.  
 XX  
 CC The invention relates to a composition comprising a substance that  
 CC modulates the status of 121PIPI (a protein encoded by a cancer expressed  
 CC gene) or a molecule that is modulated by 121PIPI where status of the cell  
 CC that expresses 121PIPI is modulated. Also included are a pharmaceutical  
 CC composition comprising the novel composition in a human unit dose form, a  
 CC recombinant protein comprising an antigen-binding region of a monoclonal  
 CC antibody, a non-human transgenic animal that produces an antibody, a  
 CC hybridoma that produces an antibody, a single chain monoclonal antibody

CC that immunospecifically binds to a 121p1f1-related protein (comprising  
CC the variable domains of the heavy and light chains of a monoclonal  
CC antibody), a vector comprising a polynucleotide that encodes a single  
CC chain monoclonal antibody, a polynucleotide that encodes an analogue  
CC peptide, delivering a cytotoxic agent or a diagnostic agent to a cell  
CC that expresses 121p1f1, inhibiting growth of cancer cells that expresses  
CC 121p1f1 (comprising administering to the cells the composition), treating  
CC a patient who bears cancer cells that express 121p1f1, generating a  
CC mammalian immune response directed to 121p1f1, inducing an immune  
CC response, monitoring 121p1f1 gene products in a biological sample from a  
CC patient who has or who is suspected of having cancer, monitoring the  
CC presence of cancer in an individual and an assay for detecting the  
CC presence of a 121p1f1-related protein or polynucleotide in a biological  
CC sample from a patient who has or who is suspected of having cancer. The  
CC composition may comprise a polynucleotide that comprises a 121p1f1-  
CC related protein coding sequence provided that the coding sequence does  
CC not encode the entire amino acid sequence of 121p1f1 (ADM83793. The  
CC substance also comprises a polynucleotide that encodes at least one  
CC peptide given in 16 Tables (given in the specification), the peptides  
CC being HLA (human leukocyte antigen)-binding epitopes from 121p1f1 or its  
CC splice variants. The composition is useful for detecting, treating or  
CC preventing cancer, preferably prostate cancer, bladder cancer, kidney  
CC cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer,  
CC cervical cancer or stomach cancer. The composition can also be used as a  
CC vaccine to treat or prevent cancer that expresses or overexpresses  
CC 121p1f1. The gene for 121p1f1 is located on chromosome 4q. The present  
CC sequence is a 121p1f1 protein (full-length or fragment).

XX Sequence 205 AA;

Query Match 100.0%; Score 1047; DB 8; Length 205;  
Best Local Similarity 100.0%; Pred. No. 1.8e-88;  
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSKKKGSAEKRRTMRMEIFSETDVPQLKLEKIAPEKIGITMSVKEVQSLVDQGMV 60  
DB 1 MSKKKGSAEKRRTMRMEIFSETDVPQLKLEKIAPEKIGITMSVKEVQSLVDQGMV 60  
QY 61 DCEKIGTSNYWAFPSKALHARKHKLFTLESQSLSEGSOKHASLQKSIKAKIGCETTER 120  
DB 61 DCEKIGTSNYWAFPSKALHARKHKLFTLESQSLSEGSOKHASLQKSIKAKIGCETTER 120  
QY 121 TRLAKESLSLDQREQLKAEVEKYKDCDPQVEVEIRQANKYAKKXANRWNTNIPAKISWA 180  
DB 121 TRLAKESLSLDQREQLKAEVEKYKDCDPQVEVEIRQANKYAKKXANRWNTNIPAKISWA 180  
QY 181 KRKGFENKIDRTFGIPEDPDYID 205  
DB 181 KRKGFENKIDRTFGIPEDPDYID 205

RESULT 8

ADM83804 ID ADM83804 standard; protein; 205 AA.

AC ADM83804;

DT 03-JUN-2004 (first entry)

XX Human cancer gene 121p1f1 protein #2.

XX Human; cancer gene 121p1f1, cytostatic; cancer; chromosome 4q; HLA;  
KW human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;  
KW colon cancer; lung cancer; pancreatic cancer; breast cancer;  
KW cervical cancer; stomach cancer; gene therapy; vaccine.

XX Homo sapiens.

PN US2003223997-A1.

PD 04-DEC-2003.

PF 28-FEB-2002; 2002US-00087190.

XX 08-FEB-2001; 2001US-00779250.

XX (CHAL/) CHALITA-EBD P M.  
PA (HUBB) HUBERT R S.  
PA (RAIT/) RAITANO A B.  
PA (FARI/) FARIS M.  
PA (AFAR/) AFAR D E H.  
PA (GEW/) GE W.  
PA (JAKO/) JAKOBOVITS A.

XX Chalitita-Elid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W;  
PI Jakobovits A;  
XX WPI; 2004-060522/06.

PT New composition comprising a substance that modulates the status of  
PT 121p1f1 or a molecule that is modulated by 121p1f1, useful for detecting,  
PT treating or preventing cancer e.g. prostate, bladder, colon, breast or  
PT lung cancer.

XX Disclosure; SEQ ID NO 14; 211p1; English.

XX The invention relates to a composition comprising a substance that  
CC modulates the status of 121p1f1 (a protein encoded by a cancer expressed  
CC gene) or a molecule that is modulated by 121p1f1 where status of the cell  
CC that expresses 121p1f1 is modulated. Also included are a pharmaceutical  
CC composition comprising the novel composition in a human unit dose form, a  
CC recombinant protein comprising an antigen-binding region of a monoclonal  
CC antibody, a non-human transgenic animal that produces an antibody, a  
CC hybridoma that produces an antibody, a single chain monoclonal antibody  
CC that immunospecifically binds to a 121p1f1-related protein (comprising  
CC the variable domains of the heavy and light chains of a monoclonal  
CC antibody), a vector comprising a polynucleotide that encodes a single  
CC chain monoclonal antibody, a polynucleotide that encodes an analogue  
CC peptide, delivering a cytotoxic agent or a diagnostic agent to a cell  
CC that expresses 121p1f1, inhibiting growth of cancer cells that expresses  
CC 121p1f1 (comprising administering to the cells the composition), treating  
CC a patient who bears cancer cells that express 121p1f1, generating a  
CC mammalian immune response directed to 121p1f1, inducing an immune  
CC response, monitoring 121p1f1 gene products in a biological sample from a  
CC patient who has or who is suspected of having cancer, monitoring the  
CC presence of cancer in an individual and an assay for detecting the  
CC presence of a 121p1f1-related protein or polynucleotide in a biological  
CC sample from a patient who has or who is suspected of having cancer. The  
CC composition may comprise a polynucleotide that comprises a 121p1f1-  
CC related protein coding sequence provided that the coding sequence does  
CC not encode the entire amino acid sequence of 121p1f1 (ADM83793. The  
CC substance also comprises a polynucleotide that encodes at least one  
CC peptide given in 16 Tables (given in the specification), the peptides  
CC being HLA (human leukocyte antigen)-binding epitopes from 121p1f1 or its  
CC splice variants. The composition is useful for detecting, treating or  
CC preventing cancer, preferably prostate cancer, bladder cancer, kidney  
CC cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer,  
CC cervical cancer or stomach cancer. The composition can also be used as a  
CC vaccine to treat or prevent cancer that expresses or overexpresses  
CC 121p1f1. The gene for 121p1f1 is located on chromosome 4q. The present  
CC sequence is a 121p1f1 protein (full-length or fragment).

XX Sequence 205 AA;

Query Match 100.0%; Score 1047; DB 8; Length 205;  
Best Local Similarity 100.0%; Pred. No. 1.8e-88;  
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSKKKGSAEKRRTMRMEIFSETDVPQLKLEKIAPEKIGITMSVKEVQSLVDQGMV 60  
DB 1 MSKKKGSAEKRRTMRMEIFSETDVPQLKLEKIAPEKIGITMSVKEVQSLVDQGMV 60  
QY 61 DCEKIGTSNYWAFPSKALHARKHKLFTLESQSLSEGSOKHASLQKSIKAKIGCETTER 120  
DB 61 DCEKIGTSNYWAFPSKALHARKHKLFTLESQSLSEGSOKHASLQKSIKAKIGCETTER 120



QY 121 TRLAKELSSLDQREQLKAEVEKTKDCDPQVVEEIRQANKVAKKANWNTDNIFAIKSWA 180  
 DB 121 TRLAKELSSLDQREQLKAEVEKTKDCDPQVVEEIRQANKVAKKANWNTDNIFAIKSWA 180  
 QY 181 KRKFGFEENKIDRTFGIPEDFDYID 205  
 DB 181 KRKFGFEENKIDRTFGIPEDFDYID 205  
 RESULT 9  
 ABP75541  
 ID ABP75541 standard; protein, 219 AA.  
 AC ABP75541;  
 DT 10-FEB-2003 (first entry)  
 XX  
 DE Human secretory polypeptide SPTM SEQ ID NO 725.  
 XX  
 KW Human; SPTM; autoimmune disorder; inflammatory disorder; AIDS; anaemia;  
 KW asthma; Crohn's disease; neurological disorder; epilepsy; cancer;  
 KW Huntington's disease; Alzheimer's disease; Creutzfeldt-Jakob disease;  
 KW multiple sclerosis; Parkinson's disease; cell proliferative disorder;  
 KW anti-inflammatory; immunosuppressive; neuroprotective; noctropic;  
 KW neuroleptic; anticonvulsant; cytostatic; antiparkinsonian; anxiolytic;  
 KW antiproliferative; antianaemic; anti-HIV; human immunodeficiency virus;  
 KW secretory polynucleotide; secretory protein.  
 XX  
 OS Homo sapiens.  
 PN MO20283876-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 27-MAR-2002; 2002MO-US0009921.  
 XX  
 PR 29-MAR-2001; 2001US-0280067P.  
 PR 29-MAR-2001; 2001US-0280068P.  
 PR 16-MAY-2001; 2001US-0291280P.  
 PR 17-MAY-2001; 2001US-0291829P.  
 PR 17-MAY-2001; 2001US-0291849P.  
 PR 19-JUN-2001; 2001US-0299428P.  
 PR 20-JUN-2001; 2001US-0299776P.  
 PR 20-JUN-2001; 2001US-0300001P.  
 XX  
 PA (INCY- ) INCYTE GENOMICS INC.  
 PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J,  
 PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PG, Ameshey SR,  
 PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH,  
 PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B,  
 PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;  
 XX  
 DR WPI; 2003-075543/07.  
 DR N-PSDB; AB235987.  
 XX  
 PT New human secretory proteins and polynucleotides, useful for diagnosing,  
 PT treating or preventing autoimmune/inflammatory disorders (e.g. AIDS),  
 PT neurological disorders (e.g. Alzheimer's), or cell proliferations or  
 PT cancers.  
 XX  
 PS Claim 27; SEQ ID NO 725; 458bp + Sequence Listing; English.  
 CC The invention relates to a secretory polynucleotide (designated sptm)  
 CC comprising any of 567 polynucleotide sequences (AB235837-AB236403), a  
 CC naturally occurring polynucleotide sequence at least 90 % identical to  
 CC the polynucleotide sequence, a polynucleotide complementary to them or an  
 CC RNA equivalent of them. The polypeptide or polynucleotide are useful for  
 CC treating, preventing or diagnosing a disease or condition associated with  
 CC the expression of functional SPTM. These are particularly useful for  
 CC diagnosing, treating or preventing autoimmune/inflammatory disorders  
 CC (e.g. acquired immunodeficiency syndrome, anaemia, asthma or Crohn's  
 CC disease), neurological disorders (e.g. epilepsy, Huntington's disease,

CC dementia, stroke, Alzheimer's disease, Creutzfeldt-Jakob disease,  
 CC multiple sclerosis, cerebral palsy, Parkinson's disease, anxiety,  
 CC schizophrenia or amnesia), or cell proliferative disorders (e.g.  
 CC psoriasis, polycythemia vera, or cancers including adenocarcinoma,  
 CC leukaemia, lymphoma, melanoma, myeloma, sarcoma or cancers of the brain,  
 CC breast, cervix or prostate). The present sequence is one of the SPTM  
 CC proteins of the invention (ABP75384-ABP75962). Note: The sequence data  
 CC for this patent did not form part of the printed specification, but was  
 CC obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 QY Sequence 219 AA;  
 XX  
 SO Query Match 100.0%; Score 1047; DB 6; Length 219;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-88;  
 Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSKKKGSLAEKRRRMMEIFSETDVPOLKLEKIAPEKGITMSVENVLSVDDGV 60  
 DB 15 MSKKKGSLAEKRRRMMEIFSETDVPOLKLEKIAPEKGITMSVENVLSVDDGV 74  
 QY 61 DCEKIGTSNYWAFPSKALHARKHLEVLSEQLSEGSQKASLQKSIKAKIGRCETBR 120  
 DB 75 DCEKIGTSNYWAFPSKALHARKHLEVLSEQLSEGSQKASLQKSIKAKIGRCETBR 134  
 QY 121 TRLAKELSSLDQREQLKAEVEKTKDCDPQVVEEIRQANKVAKKANWNTDNIFAIKSWA 180  
 DB 135 TRLAKELSSLDQREQLKAEVEKTKDCDPQVVEEIRQANKVAKKANWNTDNIFAIKSWA 194  
 QY 181 KRKFGFEENKIDRTFGIPEDFDYID 205  
 DB 195 KRKFGFEENKIDRTFGIPEDFDYID 219  
 RESULT 10  
 ADM83834  
 ID ADM83834 standard; protein, 206 AA.  
 XX  
 AC ADM83834;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Human cancer gene 121P1F1 variant protein #1.  
 KW Human; cancer gene 121P1F1; cytostatic; cancer; chromosome 4q; HLA;  
 KW human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;  
 KW colon cancer; lung cancer; pancreatic cancer; breast cancer;  
 KW cervical cancer; stomach cancer; gene therapy; vaccine.  
 OS Homo sapiens.  
 PN US2003223997-A1.  
 XX  
 PD 04-DEC-2003.  
 XX  
 PF 28-FEB-2002; 2002US-00087190.  
 XX  
 PR 08-FEB-2001; 2001US-00779250.  
 XX  
 PA (CHAL/) CHALLITA-EID P M.  
 PA (HUBE/) HUBERT R S.  
 PA (RAIT/) RAITANO A B.  
 PA (FARI/) FARIS M.  
 PA (AFAR/) AFAR D E H.  
 PA (JAKO/) JAKO W.  
 PA (JAKO/) JAKOBOVITS A.  
 PI Challita-Eid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W,  
 PI Jakobovits A;  
 XX  
 DR WPI; 2004-060522/06.  
 XX  
 PT New composition comprising a substance that modulates the status of

PT 121PI1 or a molecule that is modulated by 121PI1, useful for detecting,  
PT treating or preventing cancer e.g. prostate, bladder, colon, breast or  
PT lung cancer.

XX Example 5; SEQ ID NO 44; 211pp; English.

CC The invention relates to a composition comprising a substance that  
CC modulates the status of 121PI1 (a protein encoded by a cancer expressed  
CC gene) or a molecule that is modulated by 121PI1 where status of the cell  
CC that expresses 121PI1 is modulated. Also included are a pharmaceutical  
CC composition comprising the novel composition in a human unit dose form, a  
CC recombinant protein comprising an antigen-binding region of a monoclonal  
CC antibody, a non-human transgenic animal that produces an antibody, a  
CC hybridoma that produces an antibody, a single chain monoclonal antibody  
CC that immunospecifically binds to a 121PI1-related protein (comprising  
CC the variable domains of the heavy and light chains of a monoclonal  
CC antibody), a vector comprising a polynucleotide that encodes a single  
CC chain monoclonal antibody, a polynucleotide that encodes an analogue  
CC peptide, delivering a cytotoxic agent or a diagnostic agent to a cell  
CC that expresses 121PI1, inhibiting growth of cancer cells that expresses  
CC 121PI1 (comprising administering to the cells the composition), treating  
CC a patient who bears cancer cells that express 121PI1, generating a  
CC mammalian immune response directed to 121PI1, inducing an immune  
CC response, monitoring 121PI1 gene products in a biological sample from a  
CC patient who has or who is suspected of having cancer, monitoring the  
CC presence of cancer in an individual and an assay for detecting the  
CC presence of a 121PI1-related protein or polynucleotide in a biological  
CC sample from a patient who has or who is suspected of having cancer. The  
CC composition may comprise a polynucleotide that comprises a 121PI1-  
CC related protein coding sequence provided that the coding sequence does  
CC not encode the entire amino acid sequence of 121PI1 (ADM83793). The  
CC substance also comprises a polynucleotide that encodes at least one  
CC peptide given in 16 Tables (given in the specification), the peptides  
CC being HLA (human leukocyte antigen)-binding epitopes from 121PI1 or its  
CC splice variants. The composition is useful for detecting, treating or  
CC preventing cancer, preferably prostate cancer, bladder cancer, kidney  
CC cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer,  
CC cervical cancer or stomach cancer. The composition can also be used as a  
CC vaccine to treat or prevent cancer that expresses or overexpresses  
CC 121PI1. The gene for 121PI1 is located on chromosome 4q. The present  
CC sequence is a 121PI1 protein (full-length or fragment).

XX Sequence 206 AA;

Query Match 99.0%; Score 1036.5; DB 8; Length 206;  
Best Local Similarity 99.5%; Pred. No. 1.7e-87;  
Matches 205; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MSKKKGLSAEKKRTMWEIFSETKDVFLQKLEKTAPEKGIITAMSVKEVQLSLVDGMV 60  
DB 1 MSKKKGLSAEKKRTMWEIFSETKDVFLQKLEKTAPEKGIITAMSVKEVQLSLVDGMV 60  
QY 61 DCEKGTGNYWAFPSKALHARKHKLTVLES-QLSESGOKIASLOKSTEKKIGRCETEE 119  
DB 61 DCEKGTGNYWAFPSKALHARKHKLTVLES-QLSESGOKIASLOKSTEKKIGRCETEE 120  
QY 120 RTRIAKELSSLRDQEQKAEVEKKYKDCDPVVEEIRQANKVAKAANRMTDNIFAISW 179  
DB 121 RTRIAKELSSLRDQEQKAEVEKKYKDCDPVVEEIRQANKVAKAANRMTDNIFAISW 180  
QY 180 AKRRKGFEBNKIDRTFGIPEDFDYID 205  
DB 181 AKRRKGFEBNKIDRTFGIPEDFDYID 206

RESULT 11

ADM83835 ADM83835 standard; protein; 206 AA.

XX AC ADM83835;

DT 03-JUN-2004 (first entry)

XX

DE Human cancer gene 121PI1 variant protein #2.

XX Human; cancer gene 121PI1; cytostatic; cancer; chromosome 4q; HLA;  
XX human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;  
XX colon cancer; lung cancer; pancreatic cancer; breast cancer;  
XX cervical cancer; stomach cancer; gene therapy; vaccine.

OS Homo sapiens.

XX US2003223997-A1.

XX 04-DEC-2003.

XX 28-FEB-2002; 2002US-00087190.

XX 08-FEB-2001; 2001US-00779250.

XX (CHALITA-EBID P M.

XX (HUBERT) HUBERT R S.

XX (RAIT) RAITANO A B.

XX (FARIT) FARIS M.

XX (AFAR) AFAR D E H.

XX (GEW) GE W.

XX (JAKO) JAKOVIITS A.

XX Chalita-EBid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W,

XX Jakobovits A;

XX WPI; 2004-060522/06.

PT New composition comprising a substance that modulates the status of  
PT 121PI1 or a molecule that is modulated by 121PI1, useful for detecting,  
PT treating or preventing cancer e.g. prostate, bladder, colon, breast or  
PT lung cancer.

XX Example 5; SEQ ID NO 45; 211pp; English.  
CC The invention relates to a composition comprising a substance that  
CC modulates the status of 121PI1 (a protein encoded by a cancer expressed  
CC gene) or a molecule that is modulated by 121PI1 where status of the cell  
CC that expresses 121PI1 is modulated. Also included are a pharmaceutical  
CC composition comprising the novel composition in a human unit dose form, a  
CC recombinant protein comprising an antigen-binding region of a monoclonal  
CC antibody, a non-human transgenic animal that produces an antibody, a  
CC hybridoma that produces an antibody, a single chain monoclonal antibody  
CC that immunospecifically binds to a 121PI1-related protein (comprising  
CC the variable domains of the heavy and light chains of a monoclonal  
CC antibody), a vector comprising a polynucleotide that encodes a single  
CC chain monoclonal antibody, a polynucleotide that encodes an analogue  
CC peptide, delivering a cytotoxic agent or a diagnostic agent to a cell  
CC that expresses 121PI1, inhibiting growth of cancer cells that expresses  
CC 121PI1 (comprising administering to the cells the composition), treating  
CC a patient who bears cancer cells that express 121PI1, generating a  
CC mammalian immune response directed to 121PI1, inducing an immune  
CC response, monitoring 121PI1 gene products in a biological sample from a  
CC patient who has or who is suspected of having cancer, monitoring the  
CC presence of cancer in an individual and an assay for detecting the  
CC presence of a 121PI1-related protein or polynucleotide in a biological  
CC sample from a patient who has or who is suspected of having cancer. The  
CC composition may comprise a polynucleotide that comprises a 121PI1-  
CC related protein coding sequence provided that the coding sequence does  
CC not encode the entire amino acid sequence of 121PI1 (ADM83793). The  
CC substance also comprises a polynucleotide that encodes at least one  
CC peptide given in 16 Tables (given in the specification), the peptides  
CC being HLA (human leukocyte antigen)-binding epitopes from 121PI1 or its  
CC splice variants. The composition is useful for detecting, treating or  
CC preventing cancer, preferably prostate cancer, bladder cancer, kidney  
CC cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer,  
CC cervical cancer or stomach cancer. The composition can also be used as a  
CC vaccine to treat or prevent cancer that expresses or overexpresses  
CC 121PI1. The gene for 121PI1 is located on chromosome 4q. The present  
CC sequence is a 121PI1 protein (full-length or fragment).



Sequence 206 AA;  
Query Match 99.0%; Score 1036.5; DB 8; Length 206;  
Best Local Similarity 99.5%; Pred. No. 1.7e-87;  
Matches 205; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MSKKGLSAEERKRTMMEIFSETKOVFOUKDLEKIAPEKEGITTAMSVKEVLOSLVDGKV 60  
DB 1 MSKKGLSAEERKRTMMEIFSETKOVFOUKDLEKIAPEKEGITTAMSVKEVLOSLVDGKV 60  
QY 61 DCEKGTSTNYWAFPSKALHARKHKLVEESQ-LSRGSQKASLQKSTIKATIGCEEE 119  
DB 61 DCEKGTSTNYWAFPSKALHARKHKLVEESQ-LSRGSQKASLQKSTIKATIGCEEE 120  
QY 120 RTRLAKELSLRDQREOLKAVERKYKDCDPQVVEIRQANKVAKKANRWTNIFAISKM 179  
DB 121 RTRLAKELSLRDQREOLKAVERKYKDCDPQVVEIRQANKVAKKANRWTNIFAISKM 180  
QY 180 AKRKFGEENKIDRTFGIPEDFDYID 205  
DB 181 AKRKFGEENKIDRTFGIPEDFDYID 206

RESULT 12  
ADM83814  
ID ADM83814 standard; protein; 198 AA.  
XX  
AC ADM83814;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE Human cancer gene 121P1F1 protein fragment.  
XX  
KW Human; cancer gene 121P1F1; cytostatic; cancer; chromosome 4q; HLA;  
KW human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;  
KW colon cancer; lung cancer; pancreatic cancer; breast cancer;  
KW cervical cancer; stomach cancer; gene therapy; vaccine.  
XX  
OS Homo sapiens.  
XX  
PN US2003223997-A1.  
XX  
PD 04-DEC-2003.  
XX  
PF 28-FEB-2002; 2002US-00087190.  
XX  
PR 08-FEB-2001; 2001US-00779250.  
XX  
PA (CHAL/) CHALLITA-EID P M.  
PA (HUBE/) HUBERT R S.  
PA (RAT/) RATTANO A B.  
PA (FARI/) PARIS M.  
PA (AFAR/) AFAR D E H.  
PA (GEW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
XX  
PI Challaite-Bid PM, Hubert RS, Rattano AB, Paris M, Afar DEH, Ge W;  
PI Jakobovits A;  
XX  
DR WPI; 2004-060522/06.  
XX  
PT New composition comprising a substance that modulates the status of  
PT 121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting,  
PT treating or preventing cancer e.g. prostate, bladder, colon, breast or  
PT lung cancer.  
XX  
PS Example 2; SEQ ID NO 24; 211pp; English.  
XX  
CC The invention relates to a composition comprising a substance that  
CC modulates the status of 121P1F1 (a protein encoded by a cancer expressed  
CC gene) or a molecule that is modulated by 121P1F1 where status of the cell  
CC that expresses 121P1F1 is modulated. Also included are a pharmaceutical  
CC composition comprising the novel composition in a human unit dose form, a

recombinant protein comprising an antigen-binding region of a monoclonal  
antibody, a non-human transgenic animal that produces an antibody, a  
hybridoma that produces an antibody, a single chain monoclonal antibody  
that immunospecifically binds to a 121P1F1-related protein (comprising  
the variable domains of the heavy and light chains of a monoclonal  
antibody), a vector comprising a polynucleotide that encodes a single  
chain monoclonal antibody, a polynucleotide that encodes an analogue  
peptide, delivering a cytotoxic agent or a diagnostic agent to a cell  
that expresses 121P1F1, inhibiting growth of cancer cells that expresses  
121P1F1 (comprising administering to the cells the composition), treating  
a patient who bears cancer cells that express 121P1F1, generating a  
mammalian immune response directed to 121P1F1, inducing an immune  
response, monitoring 121P1F1 gene products in a biological sample from a  
patient who has or who is suspected of having cancer, monitoring the  
presence of cancer in an individual and an assay for detecting the  
presence of a 121P1F1-related protein or polynucleotide in a biological  
sample from a patient who has or who is suspected of having cancer. The  
composition may comprise a polynucleotide that comprises a 121P1F1-  
related protein coding sequence provided that the coding sequence does  
not encode the entire amino acid sequence of 121P1F1 (ADM83793). The  
CC substance also comprises a polynucleotide that encodes at least one  
CC peptide given in 16 Tables (given in the specification), the peptides  
CC being HLA (human leukocyte antigen)-binding epitopes from 121P1F1 or its  
CC splice variants. The composition is useful for detecting, treating or  
CC preventing cancer, preferably prostate cancer, bladder cancer, kidney  
CC cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer,  
CC cervical cancer or stomach cancer. The composition can also be used as a  
CC vaccine to treat or prevent cancer that expresses or overexpresses  
CC 121P1F1. The gene for 121P1F1 is located on chromosome 4q. The present  
CC sequence is a 121P1F1 protein (full-length or fragment).

Sequence 198 AA;  
Query Match 96.6%; Score 1011; DB 8; Length 198;  
Best Local Similarity 100.0%; Pred. No. 3.6e-85;  
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KGLSAEERKRTMMEIFSETKOVFOUKDLEKIAPEKEGITTAMSVKEVLOSLVDGKVCRR 64  
DB 1 KGLSAEERKRTMMEIFSETKOVFOUKDLEKIAPEKEGITTAMSVKEVLOSLVDGKVCRR 60  
QY 65 IGTSNYWAFPSKALHARKHKLVEESQ-LSRGSQKASLQKSTIKATIGCEERTRIA 124  
DB 61 IGTSNYWAFPSKALHARKHKLVEESQ-LSRGSQKASLQKSTIKATIGCEERTRIA 120  
QY 125 KGLSLRQREOLKAVERKYKDCDPQVVEIRQANKVAKKANRWTNIFAISKAKRKF 184  
DB 121 KGLSLRQREOLKAVERKYKDCDPQVVEIRQANKVAKKANRWTNIFAISKAKRKF 180  
QY 185 GFEENKIDRTFGIPEDFD 202  
DB 181 GFEENKIDRTFGIPEDFD 198

RESULT 13  
AAM40043  
ID AAM40043 standard; protein; 190 AA.  
XX  
AC AAM40043;  
XX  
DT 22-OCT-2001 (first entry)  
XX  
DE Human polypeptide SEQ ID NO 3188.  
XX  
KW Human; noctropic; immunosuppressant; cytostatic; gene therapy; cancer;  
KW peripheral nervous system; neuropathy; central nervous system; CNS;  
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemoclastic;  
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
KW leukaemia.  
XX  
OS Homo sapiens.  
XX

PN WO200153312-A1.  
 XX 26-JUL-2001.  
 XX 26-DEC-2000; 2000WO-US034263.  
 XX 23-DEC-1999; 99US-00471275.  
 PR 21-JAN-2000; 2000US-00468725.  
 PR 25-APR-2000; 2000US-0052317.  
 PR 20-JUN-2000; 2000US-00598042.  
 PR 19-JUL-2000; 2000US-00620312.  
 PR 03-AUG-2000; 2000US-00653450.  
 PR 14-SEP-2000; 2000US-00662191.  
 PR 19-OCT-2000; 2000US-00693036.  
 PR 29-NOV-2000; 2000US-00727344.  
 XX (HYSE-) HYSEQ INC.  
 PA Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,  
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA,  
 PI Zhou P, Goodrich R, Dimanac RT;  
 XX WPI; 2001-442253/47.  
 DR N-PSDB; AAI59199.  
 XX Novel nucleic acids and polypeptides, useful for treating disorders such  
 PT as central nervous system injuries.  
 PS Example 4; SEQ ID NO 3188; 10078pp; English.  
 XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the  
 CC encoded polypeptides (AAM36642-AAM42213) with neurotropic,  
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC of the invention may be used to treat diseases of the peripheral nervous  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and  
 CC localised neuropathies and central nervous system diseases, such as  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 CC utilisation of the activities such as: Immune system suppression,  
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukemias and  
 CC C.N.S disorders. Note: The sequence data for this patent did not form  
 CC part of the printed specification  
 XX  
 SQ Sequence 190 AA;  
 Query Match 93.1%; Score 975; DB 4; Length 190;  
 Best Local Similarity 100.0%; Pred. No. 7.3e-82;  
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 16 MMEIFSETKDVFOQLDLEKIAPEKGIITAMSVKVLQSLVDGMDVCRIQTSNYMAFP 75  
 DB 1 MMEIFSETKDVFOQLDLEKIAPEKGIITAMSVKVLQSLVDGMDVCRIQTSNYMAFP 60  
 QY 76 SKALHARKHKLVEVLSQSLSEGSGQKASLQKSIIEKAKIGRCETERTRIAKELSLRDRE 135  
 DB 61 SKALHARKHKLVEVLSQSLSEGSGQKASLQKSIIEKAKIGRCETERTRIAKELSLRDRE 120  
 QY 136 QLKAEVEKYKDCDPQVVEIRIQANKVAKAANRWTDNIFAIKSWAKRRKGFENKIDRTF 195  
 DB 121 QLKAEVEKYKDCDPQVVEIRIQANKVAKAANRWTDNIFAIKSWAKRRKGFENKIDRTF 180  
 QY 196 GIPEDFDYID 205  
 DB 181 GIPEDFDYID 190  
 RESULT 14  
 ADD84547  
 ID ADD84547 standard; protein; 190 AA.  
 XX

AC ADD84547;  
 XX 29-JAN-2004 (first entry)  
 XX 121PIPL1 variant 4 protein.  
 DE 121PIPL1; 121PIPL1 modulation; human; chromosome 4q; cytostatic;  
 KM gene therapy; vaccine; cancer; immune response; immunisation.  
 XX Synthetic.  
 OS Homo sapiens.  
 XX WO200295009-A2.  
 PM 28-NOV-2002.  
 PD 28-FEB-2002; 2002WO-US006242.  
 PR 05-MAR-2001; 2001US-00799250.  
 PA (AGEN-) AGENSYS INC.  
 PI Chailita-Bid PM, Hubert RS, Raitano AB, Farris M, Afar DEH, Ge W,  
 PI Jakobovits A;  
 XX WPI; 2003-156757/15.  
 DR N-PSDB; ADD84546.  
 XX Composition comprising a substance that modulates the status of 121PIPL1,  
 PT useful in diagnosing, preventing, prognosticating or treating patients  
 PT with cancer that expresses 121PIPL1, such as breast, colon, ovarian or  
 PS lung cancer.  
 XX Claim 19; Fig 2F; 285pp; English.  
 XX The present invention describes a composition (I) comprising a substance  
 CC that modulates the status of 121PIPL1 (gene and encoded protein), or a  
 CC molecule that is modulated by 121PIPL1, where the status of a cell that  
 CC expresses 121PIPL1 is modulated. The human 121PIPL1 gene maps to chromosome  
 CC 4q. (I) has cytostatic activity, and can be used in gene therapy, and in  
 CC vaccines. The composition (I) can be used for diagnosing, preventing,  
 CC prognosticating or treating patients with cancer that expresses 121PIPL1,  
 CC such as breast, colon, ovarian or lung cancer. The 121PIPL1 gene or its  
 CC fragment can be used to elicit a humoral or cellular immune response.  
 CC 121PIPL1 antibodies can be used in active or passive immunisation. 121PIPL1  
 CC polynucleotides are useful as probes and primers for the amplification or  
 CC detection of 121PIPL1 genes, as coding sequences for directing the  
 CC expression of 121PIPL1 polypeptides, or as tools for modulating or  
 CC inhibiting the expression of 121PIPL1 genes. The present sequence is used  
 CC in the exemplification of the present invention.  
 XX  
 SQ Sequence 190 AA;  
 Query Match 93.1%; Score 975; DB 7; Length 190;  
 Best Local Similarity 100.0%; Pred. No. 7.3e-82;  
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 16 MMEIFSETKDVFOQLDLEKIAPEKGIITAMSVKVLQSLVDGMDVCRIQTSNYMAFP 75  
 DB 1 MMEIFSETKDVFOQLDLEKIAPEKGIITAMSVKVLQSLVDGMDVCRIQTSNYMAFP 60  
 QY 76 SKALHARKHKLVEVLSQSLSEGSGQKASLQKSIIEKAKIGRCETERTRIAKELSLRDRE 135  
 DB 61 SKALHARKHKLVEVLSQSLSEGSGQKASLQKSIIEKAKIGRCETERTRIAKELSLRDRE 120  
 QY 136 QLKAEVEKYKDCDPQVVEIRIQANKVAKAANRWTDNIFAIKSWAKRRKGFENKIDRTF 195  
 DB 121 QLKAEVEKYKDCDPQVVEIRIQANKVAKAANRWTDNIFAIKSWAKRRKGFENKIDRTF 180  
 QY 196 GIPEDFDYID 205  
 DB 181 GIPEDFDYID 190

RESULT 15  
ADM83857  
ID ADM83857 standard; protein; 190 AA.  
XX  
AC ADM83857;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE Human cancer gene 121P1F1 protein 16-205.  
XX  
KW Human; cancer gene 121P1F1, cytostatic; cancer; chromosome 4q; HLA;  
KW human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;  
KW colon cancer; lung cancer; pancreatic cancer; breast cancer;  
KW cervical cancer; stomach cancer; gene therapy; vaccine.  
XX  
OS Homo sapiens.  
XX  
PN US2003223997-A1.  
XX  
PD 04-DEC-2003.  
XX  
PF 28-FEB-2002; 2002US-00087190.  
PR 08-FEB-2001; 2001US-00779250.  
XX  
PA (CHAL/) CHALLITA-EID P M.  
PA (HUBE/) HUBERT R S.  
PA (RAIT/) RAITANO A B.  
PA (FARI/) FARIS M.  
PA (AFAR/) AFAR D E H.  
PA (GEMW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
XX  
PI Chailita-Eid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W;  
PI Jakobovits A;  
XX  
DR WPI; 2004-060522/06.  
XX  
PT New composition comprising a substance that modulates the status of  
PT 121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting,  
PT treating or preventing cancer e.g. prostate, bladder, colon, breast or  
PT lung cancer.  
XX  
PS Example 5; SEQ ID NO 67; 211pp; English.  
XX  
CC The invention relates to a composition comprising a substance that  
CC modulates the status of 121P1F1 (a protein encoded by a cancer expressed  
CC gene) or a molecule that is modulated by 121P1F1 where status of the cell  
CC that expresses 121P1F1 is modulated. Also included are a pharmaceutical  
CC composition comprising the novel composition in a human unit dose form, a  
CC recombinant protein comprising an antigen-binding region of a monoclonal  
CC antibody, a non-human transgenic animal that produces an antibody, a  
CC hybridoma that produces an antibody, a single chain monoclonal antibody  
CC that immunospecifically binds to a 121P1F1-related protein (comprising  
CC the variable domains of the heavy and light chains of a monoclonal  
CC antibody), a vector comprising a polynucleotide that encodes a single  
CC chain monoclonal antibody, a polynucleotide that encodes an analogue  
CC peptide, delivering a cytotoxic agent or a diagnostic agent to a cell  
CC that expresses 121P1F1, inhibiting growth of cancer cells that expresses  
CC 121P1F1 (comprising administering to the cells the composition), treating  
CC a patient who bears cancer cells that express 121P1F1, generating a  
CC mammalian immune response directed to 121P1F1, inducing an immune  
CC response, monitoring 121P1F1 gene products in a biological sample from a  
CC patient who has or who is suspected of having cancer, monitoring the  
CC presence of cancer in an individual and an assay for detecting the  
CC presence of a 121P1F1-related protein or polynucleotide in a biological  
CC sample from a patient who has or who is suspected of having cancer. The  
CC composition may comprise a polynucleotide that comprises a 121P1F1-  
CC related protein coding sequence provided that the coding sequence does  
CC not encode the entire amino acid sequence of 121P1F1 (ADM83793). The  
CC substance also comprises a polynucleotide that encodes at least one  
CC peptide given in 16 Tables (given in the specification), the peptides

CC being HLA (human leukocyte antigen)-binding epitopes from 121P1F1 or its  
CC splice variants. The composition is useful for detecting, treating or  
CC preventing cancer, preferably prostate cancer, bladder cancer, kidney  
CC cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer,  
CC cervical cancer or stomach cancer. The composition can also be used as a  
CC vaccine to treat or prevent cancer that expresses or overexpresses  
CC 121P1F1. The gene for 121P1F1 is located on chromosome 4q. The present  
CC sequence is a 121P1F1 protein (full-length or fragment).  
XX  
SQ Sequence 190 AA;  
Query Match 93.1%; Score 975; DB 8; Length 190;  
Best Local Similarity 100.0%; Pred. No. 7.3e-82;  
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 16 MMEIFSEKDVFOAKDLEKIPKESGILTAMSVKEVLQSLVDDGVDCRIGTSNYNAFP 75  
DB 1 MMEIFSEKDVFOAKDLEKIPKESGILTAMSVKEVLQSLVDDGVDCRIGTSNYNAFP 60  
QY 76 SKALHARKHKLVELESQSLSEGSQKHAISLOKSIERAKIGRCETERTRLAKELSSIRDRE 135  
DB 61 SKALHARKHKLVELESQSLSEGSQKHAISLOKSIERAKIGRCETERTRLAKELSSIRDRE 120  
QY 136 QLKAEVEKTKCDQVWVEIRQANKVAKAANRTDNI FALKSWAKRGFEENKIDRTF 195  
DB 121 QLKAEVEKTKCDQVWVEIRQANKVAKAANRTDNI FALKSWAKRGFEENKIDRTF 180  
QY 196 GIPEDFDYID 205  
DB 181 GIPEDFDYID 190

Search completed: February 2, 2006, 12:48:42  
Job time : 63 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 2, 2006, 12:50:47 ; Search time 43 Seconds

(without alignments)  
458.708 Million cell updates/sec

Title: US-10-087-190-3

Perfect score: 1047  
Sequence: 1 MSKKKGSLSAEKRTTMEIF.....FEENKIDRTFGIPEDFDYID 205

Scoring table: BLAST62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	349	33.3	210	2 T37610	hypothetical coile
2	197	18.8	174	2 T08972	hypothetical prote
3	168.5	16.1	128	2 S61134	hypothetical prote
4	135.5	12.9	1281	2 JCS368	dynactin 1 - mouse
5	130.5	12.5	1053	2 A41642	dynactin - chicken
6	121.5	11.6	1356	2 S32763	kinectin 1 - human
7	117	11.2	768	2 T02572	hypothetical prote
8	116.5	11.1	2442	2 T08621	centrosome associa
9	115.5	11.0	880	2 F75103	conserved hypotet
10	114	10.9	284	2 S24972	tropomyosin alpha,
11	114	10.9	764	2 T05409	hypothetical prote
12	113	10.8	199	2 A32183	tropomyosin TPM1 -
13	112	10.7	284	2 JCS199	alpha-tropomyosin
14	112	10.7	285	2 A24199	tropomyosin NM, sk
15	112	10.7	559	2 S49143	EG10 protein - tad
16	112	10.7	1938	2 A59293	skeletal myosin he
17	111	10.6	559	2 A45620	cyclovillin homolog
18	111	10.6	1937	2 T18055	myosin heavy chain
19	110.5	10.6	308	2 T08796	tropomyosin - huma
20	110.5	10.6	629	2 T44607	hypothetical prote
21	110.5	10.6	879	2 C71083	conserved hypotet
22	110	10.5	284	2 I51731	alpha-tropomyosin
23	109.5	10.5	168	2 G86578	CT670 hypothetical
24	109.5	10.5	168	2 B72046	conserved hypotet
25	109.5	10.5	284	2 JCS198	alpha-tropomyosin
26	109.5	10.5	1298	2 E70318	hypothetical prote
27	109.5	10.5	1298	2 T24480	hypothetical prote
28	109.5	10.5	1390	2 S51364	sperm tail-specific
29	109	10.4	284	2 JC2551	tropomyosin alpha

30	109	10.4	284	2 S19691	tropomyosin alpha,
31	109	10.4	676	2 S00084	myosin heavy chain
32	108	10.3	670	2 F84899	hypothetical prote
33	107.5	10.3	1085	2 P66712	hypothetical prote
34	107.5	10.3	1137	2 T19414	hypothetical prote
35	107.5	10.3	1169	2 A54505	p115 homolog - Met
36	107	10.2	280	2 A22165	tropomyosin alpha
37	107	10.2	281	2 A34787	tropomyosin 1 alph
38	107	10.2	284	1 TWRBA	tropomyosin alpha
39	107	10.2	284	2 A39816	tropomyosin 2, fib
40	107	10.2	284	2 B27407	tropomyosin alpha
41	107	10.2	284	2 A25825	tropomyosin alpha
42	107	10.2	284	2 A60597	tropomyosin 2, fib
43	107	10.2	955	2 S24348	myosin heavy chain
44	106.5	10.2	746	2 T47237	myosin II heavy ch
45	106	10.1	1558	2 B71603	RESA-H3 antigen pF

#### ALIGNMENTS

##### RESULT 1

T37610 hypothetical coiled-coil protein - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

R:Hunt, S.; Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.

submitted to the EMBL Data Library, September 1995

A:Reference number: Z21730

A:Accession: T37610

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-210 <HND>

A:Cross-references: UNIPROT:Q09739; UNIPARC:UPI0000139F78; EMBL:Z54096; PDB:CAA90804.1;

A:Experimental source: strain 972h-; cosmid c13A11

A:Gene: SPDB:SPAC13A11.03

A:Map position: 1

A:Introns: 22/3

Query Match	33.3%; Score 349; DB 2; Length 210;
Best Local Similarity	41.6%; Pred. No. 3.3e-16;
Matches	84; Conservative 36; Mismatches 76; Indels 6; Gaps 5;
QY	5 KGLSAEKRTTMEIFSTKDVFOKDEKTAPEKGTAMSVKEVLQSLVDGVDGER 64
DB	4 KGLSAEKRTTMEIFSTKDVFOKDEKTAPEKGTAMSVKEVLQSLVDGVDGER 62
QY	65 IGTSNYVYAPPSKALHARKHKLKLEVSQLESGQGHASLQKSI--EKAKIGRCETE-EKT 121
DB	63 IGTSNYVYAPPSKALHARKHKLKLEVSQLESGQGHASLQKSI--EKAKIGRCETE-EKT 122
QY	122 FLAKELSLRD-QREQLKAEVKKYKDCDPQVEEIRQANKVAKAANRWTDNIFAIKSWA 180
DB	123 QYTELHAKSESLKLTQSLNLRHNCNPFELNGENTKKYMEANLMTDQIHITLAFIC 182
QY	181 KRKGFEENKIDRTFGIPEDFD 202
DB	183 -RDWGDADTQIREYCIPEDLD 203

##### RESULT 2

T08972 hypothetical protein F19B15.200 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004

C:Accession: T08972

R:Bayan, M.; Hilbert, H.; Braum, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, A.

submitted to the Protein Sequence Database, May 1999

A:Reference number: Z16519

A:Accession: T08972

A:Molecule type: DNA

A:Residues: 1-128 <BEV>  
A:Cross-references: UNIPROT:Q9S2E5; UNIPARC:UPI00000AA02; EMBL:AL078470; GSPDB:GN00062;  
A:Experimental source: cultivar Columbia; BAC clone F19B15  
C:Genetics:  
A:Gene: ATSP:F19B15.200  
A:Map position: 4  
A:Introns: 13/3; 52/3; 88/3; 109/3

Query Match  
Best Local Similarity 39.8%; Score 197; DB 2; Length 128;  
Matches 49; Conservative 23; Mismatches 37; Indels 14; Gaps 3;

Qy 16 MMEIFSTKDVFPOLKLEKIAPEKGTAVKVEYVQSLVDGMYDCERTGTSNYWAF 75  
Db 1 MLOIFVESQDFFLKLEKEMGP-KGVISQSVKVDVQSLVDVDDLVAKKIKGIS----- 52

Qy 76 SKALHARKHLEVESQSLSGSKHSLQKSIKAKTGRCTERTRLAKESLRDRE 135  
Db 53 ---LRSVQRK---LESLLQSSNKRLLAEVLDOCEALKGRSESEKTEALTLQKDIKKHK 106

Qy 136 QLK 138  
Db 107 DLK 109

RESULT 3  
S61134  
hypothenical protein YGL183c - Yeast (Saccharomyces cerevisiae)  
N:Alternate names: hypothenical protein G1604  
C:Species: Saccharomyces cerevisiae  
C:Date: 23-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 09-Jul-2004  
C:Accession: S61134; S64200  
R:Betani, I.; Coglievina, M.; Zaccaria, P.; Klima, R.; Brusch, C.V.  
submitted to the EMBL Data Library, September 1995  
A:Description: The sequence analysis of a 7.9 kb DNA fragment from the left arm of S.cer  
live new genes.  
A:Reference number: S61128  
A:Accession: S61134  
A:Molecule type: DNA  
A:Residues: 1-174 <BER>  
A:Cross-references: UNIPROT:P53102; UNIPARC:UPI000013B11A; EMBL:X91489; NID:g1143557; PI  
R:Brusch, C.V.; Coglievina, M.; Betani, I.; Klima, R.; Zaccaria, P.; Delneri, D.  
submitted to the Protein Sequence Database, May 1996  
A:Reference number: S64183  
A:Accession: S64200  
A:Molecule type: DNA  
A:Residues: 1-174 <BRU>  
A:Cross-references: UNIPARC:UPI000013B11A; EMBL:z72705; NID:g1322796; PIDN:CAA96895.1; F  
A:Experimental source: strain S288C  
C:Genetics:  
A:Gene: SGD:MND1  
A:Cross-references: SGD:S0003151  
A:Map position: 7L

Query Match  
Best Local Similarity 27.2%; Score 168.5; DB 2; Length 174;  
Matches 46; Conservative 42; Mismatches 68; Indels 13; Gaps 5;

Qy 45 MSUYEVQSLVD-DQMVDCERTGTSNYWAFPSKALHARKHLEVLQSLSGSKHSL 103  
Db 1 MIVDLVQOMIDEDVIVEKCGNINIWCFKQTLQKLYDSSLEIKKKIEVKCDIATY 60

Qy 104 OKSIEKA-KIGRCETERTRLAKESLRDREOLKAEVEKYKCDPOVEIR----- 156  
Db 61 KOELDKTLATGRRKFTYQKSYNRBALLEKKKKIQQDIKK-KNSLQKISIRMDAKI 119

Qy 157 QANK-----VAKAANRWTDNIFAIKMAKRRKGFENKIDRTFGIPDF 201  
Db 120 QENKQRIKLKKVHLEKTDNIEILIDLYKKFFLPEQIRKRFQIPDF 168

RESULT 4  
JCS368

dynactin 1 - mouse  
N:Alternate names: p150 Glued  
C:Species: Mus musculus (house mouse)  
C:Date: 28-May-1997 #sequence\_revision 18-Jul-1997 #text\_change 09-Jul-2004  
C:Accession: JCS368  
R:Jang, W.; Weber, J.S.; Tokito, M.K.; Holzbaur, E.L.F.; Meisler, M.H.  
Biochem. Biophys. Res. Commun. 231, 344-347, 1997  
A:Title: Mouse p150Glued (dynactin 1) cDNA sequence and evaluation as a candidate for th  
A:Reference number: JCS368; MUID:97223454; PMID:9070275  
A:Accession: JCS368  
A:Molecule type: mRNA  
A:Residues: 1-1281 <JAN>  
A:Cross-references: UNIPROT:O08788; UNIPARC:UPI0000027AAD; GB:U60312; NID:g2104494; PIDN  
A:Experimental source: brain  
A:Comment: This protein is a member of the oligomeric dynactin complex that is required  
C:Genetics:  
A:Gene: Dctn1  
A:Map position: 6

Query Match  
Best Local Similarity 12.9%; Score 135.5; DB 2; Length 1281;  
Matches 50; Conservative 43; Mismatches 106; Indels 15; Gaps 5;

Qy 2 SKKGLSAEKRTPMMEIFSTKDVFPOLKLEKIAPEKGTAVKVEYVQSLVDGMYD 61  
Db 279 ARKAKALEKAKRYEMEMADTADAIEMATLDKEMAEERESLQOEVBALKERVDELTTD 338

Qy 62 CER1-----GTSNYWAFPSKALHAR-KHLEVLQSLSGSKHSLQKSIK 110  
Db 339 LEIKAKIEKSGSAAISYQKLEQONARKALVRMDLSSSEQEHYKLOKMEK- 397

Qy 111 KIGRCET-ERTRLAKESLRDREOLKAEVEKYKCDPOVEIRQANKVAKAANR 168  
Db 398 KNQLELVROQRETLQSELQAEESTIDELKEQVDAALGAE-EMVEMLTDRNLIEKVE 456

Qy 169 WTDNIFAIKMAKRRKGFENKIDRTFGIPDF 202  
Db 457 LRETVDLEANNENNDYLQENARETELELRQLD 490

RESULT 5  
A41642  
dynactin - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 28-Aug-1992 #sequence\_revision 28-Aug-1992 #text\_change 09-Jul-2004  
C:Accession: A41642  
R:Gill, S.R.; Schroer, T.A.; Sillak, I.; Steyer, E.R.; Sheetz, M.P.; Cleveland, D.W.  
J. Cell Biol. 115, 1639-1650, 1991  
A:Title: Dynactin, a conserved, ubiquitously expressed component of an activator of vesl  
A:Reference number: A41642; MUID:92098576; PMID:1836789  
A:Accession: A41642  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1053 <GIL>  
A:Cross-references: UNIPROT:P35458; UNIPARC:UPI000017C003; GB:X62773; NID:g63920; PID:g6  
A:Keywords: cytoskeleton

Query Match  
Best Local Similarity 12.5%; Score 130.5; DB 2; Length 1053;  
Matches 53; Conservative 42; Mismatches 93; Indels 37; Gaps 7;

Qy 2 SKKGLSAEKRTPMMEIFSTKDVFPOLKLEKIAPEKGTAV-----SYKVEVQSLVD 57  
Db 101 AKKAKALEKAKRYEMEMADTADAIEMATLDKEMAEERASLQOEVDSLKEVEYLMD 160

Qy 58 GMV---DCERTGTSNYWAFPSKALHARKHLE---VLESQSLSG-SQKASLQKSIK 110  
Db 161 LEIKHIEIEKSGSAAISYQKLEQONARKALVRMDLSSSEKQEHYKLOKMEK 220

Qy 111 KIGRCETERTRLAKESLRDREOLKAEVEK-YKCD-----POVEIRQ 157  
Db 221 N-----TELSLQOREKLOEVEYQAKETVDELKEQVDAALGAEINVEITL 267



Qy 158 ANKYAKEANRWTDNIFAISKWAKRKGFEENKIDRTFGIPEDPD 202  
Db 268 RNLDLEEKVRELRTVGDLEAMENWDELQENARETELEREQD 312

## RESULT 6

S32763  
kinectin 1 - human  
C/Species: Homo sapiens (man)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C/Accession: S32763; I37947  
R/Kruppa, G.; Fuetterer, A.; Lemke, H.; Koenke, M.  
submitted to the EMBL Data Library, April 1993  
A/Description: Cloning and characterization of TAF, a novel transactivating protein.  
A/Reference number: S32763  
A/Accession: S32763  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-1356 <KRU>  
A/Cross-references: UNIPROT:O86UP2; UNIPARC:UPI00000702A8; EMBL:Z22551  
R/Futrerer, A.; Kruppa, G.; Kramer, B.; Lemke, H.; Kronke, M.  
Mol. Biol. Cell 6, 161-170, 1995  
A/Title: Molecular cloning and characterization of human kinectin.  
A/Reference number: I37947; MUID:95306853; PMID:7787243  
A/Accession: I37947  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-1356 <RES>  
A/Cross-references: UNIPARC:UPI00000702A8; EMBL:Z22551; NID:G2396163; PIDN:CAA80271.1; PI  
C/Genetics:  
A/Genes: GDB:KTN1  
A/Cross-references: GDB:6165852; OMIM:600653

Query Match 11.6%; Score 121.5; DB 2; Length 1356;  
Best Local Similarity 22.7%; Pred. No. 2.2;  
Matches 50; Conservative 31; Mismatches 88; Indels 51; Gaps 5;

Qy 3 KKKGLSAEKKTRMEIFSETKDVLPOLKLEKIAPEKIGTA--MSVKEVLSLVDDMV 60  
Db 1025 RKGNLDLEEKVRELRTVGDLEAMENWDELQENARETELEREQD 1084  
Qy 61 DCERIGTSNYVAPPSKALH-----ARKKLEVLSESSQKIASIQSIKAKIGRC 115  
Db 1085 P-SNLSIGEWLHGFKKAKCKGAGTSGSEEVKVLHKLKADENHTLLQLECEKYSVLA 1143  
Qy 116 ETR-----ERRRLA-XELSSRD 132  
Db 1144 ETEGILQTLQRSVEQENKMKVYKVDSEHKTKKOMQSFTSSBOELERLSKNDIENLR 1203  
Qy 133 QREOLKAEVKKKDCDDPOVVEIRQANKVAKBANRWTDN 172  
Db 1204 EREHLEMELEKAEWERSYTYVEVRELKDLTELQKLDLS 1243

## RESULT 7

T02572  
hypothenical protein At2g39300 [imported] - Arabidopsis thaliana  
N/Alternate names: hypothenical protein T16B24.6  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 09-Jul-2004  
C/Accession: T02572; F84815  
R/Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Croebly, M.L.; Brandon, R.C.; Sykes,  
submitted to the EMBL Data Library, August 1998  
A/Description: Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence.  
A/Reference number: Z14679  
A/Accession: T02572  
A/Status: translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-768 <Rou>  
A/Cross-references: UNIPROT:O80951; UNIPARC:UPI00000A1172; EMBL:AC004697; NID:G3402671;  
A/Experimental source: cultivar Columbia  
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, W.; Vanaken, S.E.; Umayam, L.; Tallon, L.

eusa, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Frazer, C.M.; Venter, J  
Nature 402, 761-768, 1999  
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A/Reference number: A84420; MUID:20083487; PMID:10617197  
A/Accession: F84815  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-768 <STO>  
A/Cross-references: UNIPARC:UPI00000A1172; GB:AE002093; NID:G3402677; PIDN:AAC28980.1; C  
C/Genetics:  
A/Genes: T16B24.6; At2g39300  
A/Map position: 2  
A/Intons: 80/2; 665/3

Query Match 11.2%; Score 117; DB 2; Length 768;  
Best Local Similarity 22.1%; Pred. No. 2.4;  
Matches 50; Conservative 46; Mismatches 90; Indels 40; Gaps 9;

Qy 1 MSKKGLSAE-----EKTRMEIFSETK-----DVFOL-KOLEKIAPEKIGT 43  
Db 247 MCKEDDVSSLEKRYKEKRVKLLSEMEKFFLSDCDFISLVGDIRQMEERVGL- 305  
Qy 44 AMSVKEVLSLVDDGMDCERIGTSNYVAPPSKALHARKKLEV-LESQSSQKIAS 102  
Db 306 AFEVLSLRQMDERASTREDIRRVKDWDLRLKLEKXTLQVLTETELDRSSWTS 365  
Qy 103 LQSGIEKAKIGRCETBERTRLAKEISLRDQEQKAEVKKDCDDPOVVEIRQANKVA 162  
Db 366 ---KVESKV-----EKKRLREKRVLEAHNVSLQRIISFHEKETERIDMIRLDET 416  
Qy 163 KE-----ANRWTDNIFAISKWAKRKGFEENKIDRTFGIPEDFDY 204  
Db 417 TELSATAEMKEENLFLMQLNLSKLSQESYT-----GSTDDLTV 454

## RESULT 8

T08621  
centrosome associated protein CEP250 - human  
C/Species: Homo sapiens (man)  
C/Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000  
C/Accession: T08621  
R/Mack, G.U.; Rees, J.; Sandblom, O.; Balczon, R.; Fritzler, M.J.; Ratner, J.B.  
Arthritis Rheum. 41, 551-558, 1998  
A/Title: Autoantibodies to a group of centrosomal proteins in human autoimmune sera reac  
A/Reference number: Z14622; MUID:98165428; PMID:9506584  
A/Accession: T08621  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-2442 <MAC>  
A/Cross-references: UNIPARC:UPI0000071A1C; EMBL:AF022655; NID:G2832236; PIDN:AAC06349.1;  
A/Experimental source: cell line HeLa

Query Match 11.1%; Score 116.5; DB 2; Length 2442;  
Best Local Similarity 19.7%; Pred. No. 9;  
Matches 46; Conservative 47; Mismatches 64; Indels 77; Gaps 8;

Qy 1 MSKKGLSAEKKTRMEIFSETKDVLPOLKLE--KIAPEKIGTAMSVKEVLSLVDDG 58  
Db 1662 LQKRIQVLEDRQRTQRTILSE-----DLQIKLSLRERGRLETTQROLMQRRABG 1713  
Qy 59 M-----VDCB-----RIGTSNYW 72  
Db 1714 KGPSKAKQSGLEHMKLLIRDKKEVCEQEHINHELQELKDLQEQLOGIHKRVGT----- 1769  
Qy 73 AFPSKALHARKKLEVLSESSQSS-----GSQKIASIQSIKAKIGRCETBERTRLAKIS 128  
Db 1770 ---SLLSQREGEIVLQOQLQEARQEGELQSGISQSLDQALQORDQ-----ELE 1820  
Qy 129 SLRQREOLKAEVKKKDCDDPOVVEIRQANKVAKBANRWTDNIFAISKWAKR 182  
Db 1821 ALQDQQAQDQEEKVKSKADALQALQALQAMTTLKERIGELQD---KEQAKR 1870

RESULT 9  
F75103  
Conserved hypothetical protein PAB0812 - Pyrococcus abyssi (strain Orsay)  
C/Species: Pyrococcus abyssi  
C/Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004  
C/Accession: F75103  
R/Anonymous, Genoscope  
Submitted to the EMBL Data Library, July 1999  
A/Description: Pyrococcus abyssi genome sequence; insights into archaeal chromosome stru  
A/Reference number: A75001  
A/Accession: F75103  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-880 <KAM>  
A/Cross-references: UNIPROT:Q9U2C8; UNIPARC:UPI0000034523; GB:AJ248286; GB:AL096836; NID  
A/Experimental source: strain Orsay  
C/Genetics:  
A/Gene: PAB0812  
C/Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF1032

Query Match 11.0%; Score 115.5; DB 2; Length 880;  
Best Local Similarity 24.1%; Pred. No. 3.5;  
Matches 58; Conservative 38; Mismatches 78; Indels 67; Gaps 10;

Oy 3 KKKGL-----SABEKTRMMEIFSETKDVDFOLKLEKIAPKKGITAMSVKYLQS 53  
Db RKKGLEEKIVQIERSIEKKAKISLEIIVDIPLOEKEKEVKLNGFR----- 306  
Oy 54 LVDDGMVDCERIGTSNYWAFPSKAL-----HAKHKLVLVSQSGSGOKHSL-- 103  
Db 307 --DEYSEKRLRLEKLSWESELKAEVIEKGEKKRAEIRNEKSEIEKRLBELKPY 364  
Oy 104 -----OKSIEKAK-----IGRCET--EERTLAKELSL-----RD 132  
Db 365 VEELEDKQVOKQIETRLKARLKGSPGVIRKLSLEKREIEBAIEITTRIGQMOGE 424  
Oy 133 QREOLKA--EVEKXKDCDPQVVEIRQANKVAKAANWTNIFAIKSMARKEGFEEENK 190  
Db 425 KNERKAIIEIRKAKGKCPVCGRELTEBHK--KEIMERYTLIYKIEBELKRTTE--BERK 481  
Oy 191 I 191  
Db 482 L 482

RESULT 10  
S24972  
tropomyosin alpha, cardiac - pig  
C/Species: Sus scrofa domestica (domestic pig)  
C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C/Accession: S24972  
R/Whitby, F.G.; Kent, H.M.; Stewart, F.; Stewart, M.; Xie, X.; Hatch, V.; Cohen, C.; Phil  
Submitted to the EMBL Data Library, April 1992  
A/Description: Structure of tropomyosin at 9 Angstroms resolution.  
A/Reference number: S24972  
A/Accession: S24972  
A/Molecule type: mRNA  
A/Status: preliminary  
A/Residues: 1-284 <WHI>  
A/Cross-references: UNIPROT:P42639; UNIPARC:UPI000013724F; EMBL:X66274; NID:g1926; PIDN:  
A/Superfamily: tropomyosin  
C/Keywords: cardiac muscle; heart

Query Match 10.9%; Score 114; DB 2; Length 284;  
Best Local Similarity 23.2%; Pred. No. 1.3;  
Matches 52; Conservative 37; Mismatches 61; Indels 74; Gaps 11;

Oy 1 MSKKKGSLAE---EKRTMMEIFSETKDVDFOLKLEKIAPKKGITAMSVKYLQSLVDD 57  
Db 73 LAEKATATAEADVASLNRIQLFEELDRAQ-----ERLA-----TALQKEBAKADK 122  
Oy 58 ---GMVDCERIGTSNYWAFPSKALHAR---KHLLEVLSQSGSGOKH----- 100

Db 123 SERGM-----KYIESRAQDERKMEIQEIQLEA--KHIAEDADKYE 163  
Oy 101 -----ASLOKSEKAKI--GRCTEERTRLATLSSLRDQFOLKAEVKKYDCD 148  
Db 164 EVARKVLVISIDLERABERABLSGKC-----AELEELKVTNTNLSLEKQAEKYGQKE 218  
Oy 149 PQVVEIRQANKVAKAANWTNIFAIKSMARKEGFEEENKID 192  
Db 219 DKVEEIKVLSDLKEAEETR-----AEFAERSVTLEKSID 254

RESULT 11  
T05409  
hypothetical protein F10M6.170 - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C/Accession: T05409  
R/Beyan, M.; Weichselgartner, M.; Partmann, B.; Grandenath, K.; Dauner, D.; Herzl, A.; N  
Submitted to the Protein Sequence Database, February 1998  
A/Reference number: Z15414  
A/Accession: T05409  
A/Molecule type: DNA  
A/Residues: 1-764 <BBV>  
A/Cross-references: UNIPROT:O49371; UNIPARC:UPI0000047B02; EMBL:AL021811  
A/Experimental source: cultivar Columbia; BAC clone F10M6  
C/Genetics:  
A/Map position: 4  
A/Note: F10M6.170

Query Match 10.9%; Score 114; DB 2; Length 764;  
Best Local Similarity 22.8%; Pred. No. 3.7;  
Matches 42; Conservative 40; Mismatches 78; Indels 24; Gaps 5;

Oy 8 SABEKTRMMEIFSETKDVDFOLKLEKIAPKKE-----GITAMSVKYLQSLV--DDG 58  
Db 49 SAESANVLFDKLPARTLRRLERQNGHVYPDDDLPSNGLVLSDEALVALLKREED 108  
Oy 59 MVDCERIGTSNYWAFPSKALHARKHKLVLVSQSGSGQHASLQKSEIKAKIGRCETE 118  
Db 109 LHDARLKLLSD-----KNKLNRAKEELEREKRTISASLGHESLOEELKXANY---ELA 159  
Oy 119 ERTLAKELSLRQFOLKAEVKKYDCDPQVVEIRQANKVAKAANWTNIFAIKS 178  
Db 160 SQAREIEELKHLKERDEERALLQSSLTKEEELKKRQ-----ETANRKEVSMALSE 213  
Oy 179 WAKR 182  
Db 214 FESK 217

RESULT 12  
A32183  
tropomyosin TPML - yeast (Saccharomyces cerevisiae)  
N/Alternate names: protein N2332; protein YN1079C  
C/Species: Saccharomyces cerevisiae  
C/Date: 08-Sep-1989 #sequence\_revision 08-Sep-1989 #text\_change 31-Dec-2004  
C/Accession: A32183; S53899; S63011; S63018; S63928  
R/Liu, H.; Bretscher, A.  
Cell 57, 233-242, 1989  
A/Title: Disruption of the single tropomyosin gene in yeast results in the disappearance  
A/Reference number: A32183; MUID:89195234; PMID:2649250  
A/Accession: A32183  
A/Molecule type: DNA  
A/Residues: 1-199 <LIU>  
A/Cross-references: UNIPROT:P17536; UNIPARC:UPI0000137254; EMBL:M25501; NID:g173037; PLOC:  
R/Poehlmann, R.; Philippen, P.  
Submitted to the EMBL Data Library, April 1995  
A/Reference number: S53896  
A/Accession: S53896  
A/Molecule type: DNA  
A/Residues: 1-199 <POE>  
A/Cross-references: UNIPARC:UPI0000137254; EMBL:X86470; NID:g791101; PIDN:CAA60179.1; PI:  
R/Poehlmann, R.; Philippen, P.

submitted to the Protein Sequence Database, April 1996  
 A:Reference number: S62997  
 A:Accession: S63011  
 A:Molecule type: DNA  
 A:Residues: 1-199 <POM>  
 A:Cross-references: UNIPARC:UPI0000137254; EMBL:Z71355; NID:G1301970; PIDN:CAA95953.1; F  
 A:Experimental source: strain S288C  
 A:Solter-Mira, A.; Salt, J.E.; Ballesta, J.P.G.; Remacha, M.  
 submitted to the Protein Sequence Database, April 1996  
 A:Reference number: S63018  
 A:Accession: S63018  
 A:Molecule type: DNA  
 A:Residues: 1-199 <SO>  
 A:Cross-references: UNIPARC:UPI0000137254; EMBL:Z71355; NID:G1301970; PIDN:CAA95953.1; F  
 A:Experimental source: strain S288C  
 A:Poehlmann, R.; Philippsen, P.  
 Yeast 12, 391-402, 1996  
 A:Title: Sequencing a cosmid clone of *Saccharomyces cerevisiae* chromosome XIV reveals 12  
 A:Reference number: S63925; MUID:96267764; PMID:8701611  
 A:Accession: S63928  
 A:Molecule type: DNA  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Residues: 1-199 <POF>  
 A:Cross-references: UNIPARC:UPI0000137254; EMBL:X86470; NID:G791101; PIDN:CAA60179.1; PI  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995  
 C:Genetics:  
 A:Gene: SGD:TPM1  
 A:Cross-references: SGD:S0005023; MIPS:YNL079c  
 A:Map position: 14L  
 C:Superfamily: slime mold ribozyme I  
 C:Keywords: coiled coil; cytoskeleton

Query Match 10.8%; Score 113; DB 2; Length 199;  
 Best Local Similarity 24.7%; Pred. No. 1;  
 Matches 46; Conservative 40; Mismatches 54; Indels 46; Gaps 8;  
 QY 7 LSAEKRTRMEIFSETKQVDFQKLEKIAPEKIGITAMSVKVLQSLVDD-----GMV 60  
 DB 13 LEASWQKYEKELKKNKDLQ-ENVE-----KENGIKSLTYKN--QLEDEIKLEAGLS 65  
 QY 61 DCEIRIGTSNYWAFPSKALHARKHL-----EVLSEQLSEG-----SOK 99  
 DB 66 DSKQTEQNVKENGQIKSLTYKNHQLBEIEIKLELAEKSLSESHHLSQNNDNFSSK 125  
 QY 100 HASLOKSEKAKIGRCETFEERTR-----LAKLSLDRORGLKAEV-----KYDC 147  
 DB 126 NQQLBEDLESQDYKLTETKLRRESDLKADQLERRVALLERQREWERKNEELTYKVEDA 185  
 QY 148 DPQVE 153  
 DB 186 KKEIDE 191

RESULT 13  
 JC6199  
 alpha-tropomyosin S-1 - axolotl  
 C:Species: *Ambystoma mexicanum* (axolotl)  
 C:Date: 11-Apr-1997 #sequence\_revision 09-May-1997 #text\_change 09-Jul-2004  
 C:Accession: JC6199  
 R:Luque, E.A.; Spilner, B.J.; Dube, S.; Dube, D.K.; Lemanski, L.F.  
 Gene 185, 175-180, 1997  
 A:Title: Differential expression of a novel isoform of alpha-tropomyosin in cardiac and  
 A:Reference number: JC6198; MUID:97208870; PMID:9055812  
 A:Contents: skeletal muscle  
 A:Accession: JC6199  
 A:Molecule type: mRNA  
 A:Residues: 1-284 <LUD>  
 A:Cross-references: UNIPROT:P87349; UNIPARC:UPI00000FBSF3; GB:U33450; NID:G1871357; PIDN  
 C:Comment: This protein is a actin-binding protein.  
 C:Genetics:  
 A:Gene: ATMS-1  
 C:Superfamily: tropomyosin  
 C:Keywords: actin binding

Query Match 10.7%; Score 112; DB 2; Length 284;  
 Best Local Similarity 22.7%; Pred. No. 1.7;  
 Matches 48; Conservative 41; Mismatches 74; Indels 48; Gaps 9;  
 QY 1 MSKKKGLSAEK---KRTRMETIFSETKQVDFQ-----LKDEIKAPK-EKGITAMSV 47  
 DB 73 LARKKADAEEDVASLNRIQLVEEELDRAPQERLATLQLEKAEKADSEBRGKVTEN 132  
 QY 48 KEVLQSLVDGMDVCERIGTSNYWAFPSKALHARKHLVLESLSEGSQK---HNSL 103  
 DB 133 R-----ALKDEKMEQLQEI-----QLQEKHIAEADRYEAVARKLVITEBDL 176  
 QY 104 QKSIKAXI--GRCEETERTLAKELSLDRQRLKAEVEKYKDCDPQVVEIRQANKV 161  
 DB 177 ERAEERAEISGKC-----ALEEELKVTNNLSLEQAQKYSQKEDKYEIEIKVLTDC 231  
 QY 162 AKPAANRTDNIFAIKSWAKKFGFEENKID 192  
 DB 232 LKEAEIR-----AEFAERTVAKLEKSID 254

RESULT 14  
 A24199  
 tropomyosin NM, skeletal muscle - human  
 C:Species: *Homo sapiens* (man)  
 C:Date: 02-Jun-1988 #sequence\_revision 02-Jun-1988 #text\_change 13-Aug-1999  
 C:Accession: S06210; A24199  
 R:Clayton, L.; Reinach, F.C.; Chumley, G.M.; Macleod, A.R.  
 J. Mol. Biol. 201, 507-515, 1988  
 A:Title: Organization of the htm(nm) gene. Implications for the evolution of muscle and  
 A:Reference number: S02554; MUID:88332987; PMID:3418707  
 A:Accession: S06210  
 A:Status: not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-285 <CLA>  
 A:Cross-references: UNIPARC:UPI000013D90D  
 R:Reinach, F.C.; Macleod, A.R.  
 Nature 322, 648-650, 1986  
 A:Title: Tissue-specific expression of the human tropomyosin gene involved in the genera  
 A:Reference number: A24199; MUID:86311274; PMID:3018581  
 A:Accession: A24199  
 A:Molecule type: mRNA  
 A:Residues: 1-285 <REI>  
 A:Cross-references: UNIPARC:UPI000013D90D; GB:X04201; NID:G37429; PIDN:CAA27798.1; PID:G  
 A:Note: an intronless pseudogene resembling this mRNA is also known  
 C:Superfamily: tropomyosin  
 C:Keywords: alternative splicing; coiled coil; muscle; skeletal muscle

Query Match 10.7%; Score 112; DB 2; Length 285;  
 Best Local Similarity 23.5%; Pred. No. 1.7;  
 Matches 52; Conservative 41; Mismatches 72; Indels 56; Gaps 9;  
 QY 1 MSKKKGLSAEK---KRTRMETIFSETKQVDFQ-----LKDEIKAPK-EKGITAMSV 47  
 DB 74 LAEKKAADAEAEVSLNRIQLVEEELDRAPQERLATLQLEKAEKADSEBRGKVTEN 133  
 QY 48 KEVLQSLVDGMDVCERIGTSNYWAFPSKALHARKHLVLESLSEGSQK---HNSL 107  
 DB 134 R-----ALKDEKMEQLQEI-----QLQEKHIAEADRYEAVARKLVITEBDL 177  
 QY 108 EKAKIGRCETERTRLA-----KELSLDRQRLKAEVEKYKDCDPQVVEIRQANKV 159  
 DB 178 ER-----TEBRKELASKSELEELKVTNNLSLEQAQKYSQKEDKYEIEIKVLT 230  
 QY 160 KVAKPAANRTDNIFAIKSWAKKFGFEENKIDRTFGIPED 200  
 DB 221 DKLKEAEIRAE---FAERSVA-----KLEKTIIDLED 259

RESULT 15  
 G49143  
 Egl10 protein - tapeworm (*Echinococcus granulosus*)

C:Species: Echinococcus granulosus  
 C:Date: 16-Feb-1995 #sequence\_revision 12-May-1995 #text\_change 15-Mar-2004  
 C:Accession: S49143  
 R:Frosch, P.M.; Hartmann, M.; Sygulla, L.; Margutti, P.; Frosch, M.  
 submitted to the EMBL Data Library, January 1994  
 A:Description: Identification of a cDNA clone from the larval stage of Echinococcus gran  
 A:Reference number: S49143  
 A:Accession: S49143  
 A:Status: Preliminary  
 A:Molecule type: mRNA  
 A:Releases: 1-559 <PRO>  
 A:Cross-references: UNIPARC:UPI0000078113; EMBL:Z29489; NID:G509759; PIDD:CA82625.1; PI  
 C:Superfamily: ezrin/radixin/moesin; protein 4.1 membrane-binding domain homology  
 F:12-293/Domain: protein 4.1 membrane-binding domain homology <B41>

Query Match 10.7%; Score 112; DB 2; Length 559;  
 Best Local Similarity 27.8%; Pred. No. 3.6;  
 Matches 49; Conservative 34; Mismatches 61; Indels 32; Gaps 7;

QY 1 MSKKKGSAEERKTRMEIFSETKDVFQKDLKIAPEKGIITMSVKEVLQSLVDDGMV 60  
 Db 294 MRRKRSDSIEYQOMKI-----QAKERELKEAERQRLKERLQRMENEOKLELRAQ-MV 347  
 QY 61 DCEKIGTSNYTWAPPSKALHARKHKLVELESQLSF-----GSQKHA--SIQKSTEK-AKI 112  
 Db 348 EKE-----SDLADMKNKASAYESKIAELEMLQOERHARESLQKSDKLAEM 394  
 QY 113 GRCEETERTRLAKELSLRDQREOLKAVEKVKDCDPQVEEIRQANKVAKKAANR 168  
 Db 395 NRKLKERTTAAAEERKRLMAQRDEVQREVEAK-----VAAKKEAEKQAQAEAEIR 445

Search completed: February 2, 2006, 12:51:41  
 Job time : 45 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 2, 2006, 12:48:52 ; Search time 119 Seconds

(without alignments)  
1215.406 Million cell updates/sec

Title: US-10-087-190-3

Perfect score: 1047

Sequence: 1 MSKKKGASAEKRTIMEIF.....FEENKIDRTFGIPEDPYID 205

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1047	100.0	205	2	Q9BWT6 HUMAN
2	954	91.1	205	2	Q8K396 MOUSE
3	948	90.5	205	2	Q9D0A1 MOUSE
4	848	81.0	205	2	Q5FV93 XENTR
5	848	81.0	205	2	Q5XGY9 XENLA
6	783	74.8	204	2	Q4S066 TETNG
7	644	61.5	220	2	Q6DC61 BRARE
8	462	44.1	196	2	Q86E28 SCHJA
9	459	43.8	269	2	Q50VW2 ENTHI
10	440	42.0	230	2	Q8GYD2 ARATH
11	427	40.8	207	2	Q6H432 ORYZA
12	366	35.0	221	2	Q54E86 DICDI
13	362	34.6	161	2	Q5BYT3 SCHJA
14	349	33.3	210	1	MCPT7 SCRO
15	340.5	32.5	203	2	Q8SUA9 ENCCU
16	340.5	32.5	203	2	Q6WDA3 GIALA
17	340.5	32.5	203	2	Q7QTX0 GIALA
18	332.5	31.8	179	2	Q6Q9F9 ASDAE
19	303	28.9	205	2	Q5S5F7 CRANE
20	277	26.5	196	2	Q7RH53 PLAYO
21	266.5	25.5	211	2	Q6BQUS DERBA
22	224.5	21.4	299	2	Q5KCA2 CRINE
23	221	21.1	225	2	Q7SCH5 ASHGO
24	213	20.3	427	2	Q4QAN2 LBIWA
25	206.5	19.7	225	2	Q6CSX5 KULIA
26	202.5	19.3	221	2	Q5BCH7 EMENT
27	197	18.8	128	2	Q8SZB5 ARATH
28	191.5	18.3	201	2	Q59RP1 CANAL
29	176.5	16.9	189	2	Q4WPL0 ASPFU
30	175	16.7	222	2	Q6FL56 CANGA
31	168.5	16.1	174	1	YGT3_YEAST

32	155.5	14.9	66	2	Q6CSY4 CRYPV	Q6CSY4 cryptospori
33	153.5	14.7	101	2	Q6E679 ANTLO	Q6E679 antonospora
34	136.5	13.0	910	2	Q7T2F8 BRARE	Q7T2F8 brachydantio
35	136	12.9	1395	2	Q4SSB9 TETNG	Q4SSB9 tetradon n
36	135.5	12.9	1281	1	DYNA_MOUSE	008788 mus musculu
37	134.5	12.8	459	2	Q59F36 HUMAN	Q59F36 homo sapien
38	134.5	12.8	890	2	Q6AWB1 HUMAN	Q6AWB1 homo sapien
39	134.5	12.8	890	2	Q6AWB3 HUMAN	Q6AWB3 homo sapien
40	134.5	12.8	1139	2	Q6IQ37 HUMAN	Q6IQ37 homo sapien
41	134.5	12.8	1264	2	Q6NZM3 MOUSE	Q6NZM3 mus musculu
42	134.5	12.8	1278	1	DYNA_HUMAN	Q14203 homo sapien
43	134.5	12.8	1278	2	Q6MZ73 HUMAN	Q6MZ73 homo sapien
44	131.5	12.6	1009	2	Q5RDS4_PONPY	Q5RDS4 pongo pygma
45	131.5	12.6	1280	1	DYNA_RAT	P28023 rattus norv

#### ALIGNMENTS

RESULT 1  
Q9BWT6\_HUMAN PRELIMINARY; PRT; 205 AA.  
ID Q9BWT6\_HUMAN PRELIMINARY; PRT; 205 AA.  
AC Q9BWT6\_HUMAN PRELIMINARY; PRT; 205 AA.  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)  
DE GAJ.  
GN Name=GAJ;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
OC Homo.  
OX NCB1\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Solis G., Hofer H.W.;  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lymph;  
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bonak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Heltan E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lymph;  
RA Director MGC Project;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY028916; AA26168.1; -, mRNA.  
DR EMBL; BC032142; AA32142.1; -, mRNA.  
DR Insembl; ENSG00000121211; Homo sapiens.  
DR InertPro; IPR005647; Mnd1.  
DR Pfam; PF03962; Mnd1; 1.  
SQ SEQUENCE 205 AA; 23753 MW; 95B0B14068DA0B51 CRC64;

Query Match 100.0%; Score 1047; DB 2; Length 205;  
 Best Local Similarity 100.0%; Pred. No. 8e-57;  
 Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MSKKKGSAEKKRRMMEIFSETKDVPOLKDEKIAPEKGIITMSVKEVQLSLVDDGMV	60
Db	1	MSKKKGSAEKKRRMMEIFSETKDVPOLKDEKIAPEKGIITMSVKEVQLSLVDDGMV	60
Qy	61	DCERIGTSNYWAPPSKALHARKHLEVLSEQLSESGQKHA5LQKSIKAKIGRCETEE	120
Db	61	DCERIGTSNYWAPPSKALHARKHLEVLSEQLSESGQKHA5LQKSIKAKIGRCETEE	120
Qy	121	TRLAKEISLSDQEQKAEVEKTKDCDPQVVEIRQANKVAKAANRWNTNIFAISWA	180
Db	121	TRLAKEISLSDQEQKAEVEKTKDCDPQVVEIRQANKVAKAANRWNTNIFAISWA	180
Qy	181	KRKGFESNKIDRTFGIPEDFDYID 205	
Db	181	KRKGFESNKIDRTFGIPEDFDYID 205	

## RESULT 2

Q8K396\_MOUSE

ID Q8K396\_MOUSE PRELIMINARY; PRT; 205 AA.

AC Q8K396

DT 01-OCT-2002 (TREMBlrel. 22, Created)

DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)

DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

DE GAF protein.

GN Name=2610034E18R1k;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

R1 NUCLEOTIDE SEQUENCE.

RP STRAIN=C2ECH II;

RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shemmer C.M., Schuler G.D.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Datchenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uadiri T.B., Toshlyuki S., Carninci P., Prange C.,

RA Bork S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fealy J., Heltan E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rastinejad F., Kiryushnik M.I., Skalska U., Smalins D.E.,

RA "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [2]

R1 NUCLEOTIDE SEQUENCE.

RP STRAIN=C2ECH II;

RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;

RA Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC027741; AAH27741.1; - mRNA.

DR Ensembl; ENSMUSG00000033752; Mus musculus.

DR MGI; MGI:1924165; 2610034E18R1k.

DR InterPro; IPR005647; Mnd1.

DR Pfam; PF03962; Mnd1.1

SQ SEQUENCE 205 AA; 23849 MW; 122C3FA94345120 CRC64;

Query Match 91.1%; Score 954; DB 2; Length 205;  
 Best Local Similarity 89.8%; Pred. No. 4.1e-51;  
 Matches 184; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

Qy	1	MSKKKGSAEKKRRMMEIFSETKDVPOLKDEKIAPEKGIITMSVKEVQLSLVDDGMV	60
Db	1	MSKKKGSAEKKRRMMEIFSETKDVPOLKDEKIAPEKGIITMSVKEVQLSLVDDGMV	60
Qy	61	DCERIGTSNYWAPPSKALHARKHLEVLSEQLSESGQKHA5LQKSIKAKIGRCETEE	120
Db	61	DCERIGTSNYWAPPSKALHARKHLEVLSEQLSESGQKHA5LQKSIKAKIGRCETEE	120
Qy	121	TRLAKEISLSDQEQKAEVEKTKDCDPQVVEIRQANKVAKAANRWNTNIFAISWA	180
Db	121	AMLAKESLSDQEQKAEVEKTKDCDPQVVEIRQANKVAKAANRWNTNIFAISWA	180
Qy	181	KRKGFESNKIDRTFGIPEDFDYID 205	
Db	181	KRKGFESNKIDRTFGIPEDFDYID 205	

## RESULT 3

Q9D0A1\_MOUSE

ID Q9D0A1\_MOUSE PRELIMINARY; PRT; 205 AA.

AC Q9D0A1

DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

DE Mus musculus 10 days embryo whole body cDNA, RIKEN full-length

DE enriched library, clone:2610034E18 product:GAF homolog.

GN Name=2610034E18R1k;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

R1 NUCLEOTIDE SEQUENCE.

RP STRAIN=C57BL/6J; TISSUE=Whole body;

RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RX MEDLINE=21085660; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RA Carninci P., Hayashizaki Y.;

RA "High-efficiency full-length cDNA cloning."

RA Mech. Enzymol. 303:19-44 (1999).

RL [2]

R1 NUCLEOTIDE SEQUENCE.

RP STRAIN=C57BL/6J; TISSUE=Whole body;

RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RX MEDLINE=21085660; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Atkawa T., Hara A., Fukunishi Y., Komori H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochava H.,

RA Kuhl P., Lewis S., Matsuo Y., Nikaido I., Peele G., Quackenbush J.,

RA Schirni L.M., Steubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Bojelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Casavant T.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima U., Mazzaletti J., Mombere P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,

RA Watanabe-Borita A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection."

RL Nature 409:685-690 (2001).

RN [3]

R1 NUCLEOTIDE SEQUENCE.

RP STRAIN=C57BL/6J; TISSUE=Whole body;

RC The FANTOM Consortium;

RA The RIKEN Genome Exploration Research Group Phase I &amp; II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of



RT 60,770 full-length cDNAe.";  
RL Nucleotide 420:563-573(2002).  
[4]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Whole body;  
RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
[5]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Whole body;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,  
RA Kono H., Akiyama J., Nishi K., Katsunaka T., Teshiro H., Itoh M.,  
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multichannel sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
[6]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Whole body;  
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,  
RA Akakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,  
RA Imetani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,  
RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,  
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ono M.,  
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,  
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,  
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,  
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
RA Muramatsu M., Hayashizaki Y.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK011664; BAB27765.1; -; mRNA.  
DR Ensembl; ENSMUSG00000033752; Mus musculus.  
DR MGI; MGI:1924165; 2610034E18Rik.  
DR InterPro; IPR005647; Mnd1.  
DR Pfam; PF03962; Mnd1; 1  
SQ SEQUENCE 205 AA; 23909 MW; 09368E19E4224021 CRC64;  
Query Match 90.5%; Score 948; DB 2; Length 205;  
Best Local Similarity 89.3%; Pred. No. 9,6e-51;  
Matches 183; Conservative 10; Mismatches 12; Indels 0; Gaps 0;  
QY 1 MSKKKGLSABERKTRMEIFSETKQVFPOLKLEKIAPEKGTITANSVKEVLSVDDGV 60  
DB 1 MSKKRGLSGEERKTRMEIFSETKQVFPOLKLEKIAPEKGTITANSVKEVLSVDDGV 60  
QY 61 DCEKGTNNYWAFFSKLHARKHLETLSEQLSGSQKHSLOKISIKAKIGRCEETER 120  
DB 61 DCEKGTNNYWAFFSKLHARKHLETLSEQLSGSQKHSLOKISIKAKIGRCEETER 120  
QY 121 TRIAKETSLSDQEQALAEVEKYKDCPOVEEIRIANKVAKAEANWTNDIPIAKSWA 180  
DB 121 AMLAKELSPFDQKQALAEVEKYKRECPQVVEEIRIANKVAKAEANWTNDIPIAKSWA 180  
QY 181 KRKGFEEENKIDRTFGIPEDPDYID 205  
DB 181 KRKGFEEESKIDKNGIPEDPDYID 205  
RESULT 4  
Q5FV93\_XENTR PRELIMINARY; PRT; 205 AA.  
ID Q5FV93\_XENTR PRELIMINARY; PRT; 205 AA.  
AC Q5FV93;  
DT 10-MAY-2005 (Tremblrel. 30, Created)

DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)  
DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)  
DE MGC97859 protein.  
GN Name=MGC97859;  
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
OC Xenoipodine; Xenopus; Silurana.  
OX NCBI\_TaxID=8364;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Embryo.  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diachenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Boak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.V., Lu X., Gibbs R.A.,  
RA Fahy J., Heltan E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whitting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butlerfield Y.S.N., Krzywinski M.T., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Embryo.  
RX Klein S., Gerhardt D.S.;  
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC090139; AAH90139.1; -; mRNA.  
DR InterPro; IPR005647; Mnd1.  
DR Pfam; PF03962; Mnd1; 1  
SQ SEQUENCE 205 AA; 24130 MW; 4F47091BF3BBF00A CRC64;  
Query Match 81.0%; Score 848; DB 2; Length 205;  
Best Local Similarity 77.1%; Pred. No. 1.3e-44;  
Matches 158; Conservative 29; Mismatches 18; Indels 0; Gaps 0;  
QY 1 MSKKKGLSABERKTRMEIFSETKQVFPOLKLEKIAPEKGTITANSVKEVLSVDDGV 60  
DB 1 MSKKRGLSGEERKTRMEIFSETKQVFPOLKLEKIAPEKGTITANSVKEVLSVDDGV 60  
QY 61 DCEKGTNNYWAFFSKLHARKHLETLSEQLSGSQKHSLOKISIKAKIGRCEETER 120  
DB 61 DCEKGTNNYWAFFSKLHARKHLETLSEQLSGSQKHSLOKISIKAKIGRCEETER 120  
QY 121 TRIAKETSLSDQEQALAEVEKYKDCPOVEEIRIANKVAKAEANWTNDIPIAKSWA 180  
DB 121 SKLAEELSRHRRKEELAEVEKYKDCPDVIEEIRIANKVAKAEANWTNDIPIAKSWA 180  
QY 181 KRKGFEEENKIDRTFGIPEDPDYID 205  
DB 181 KRKGFEEERQIDKNGIPEDPDYID 205  
RESULT 5  
Q5XGY9\_XENTLA PRELIMINARY; PRT; 205 AA.  
ID Q5XGY9\_XENTLA PRELIMINARY; PRT; 205 AA.  
AC Q5XGY9;  
DT 25-OCT-2004 (Tremblrel. 28, Created)  
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)  
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)  
DE LOC95113 protein.  
GN Name=LOC95113;

OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
 OC Xenopodidae; Xenopus; Xenopus.  
 NCBI\_TaxId=8355;  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Ovary;  
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
 RA Klein S.L., Strassberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 Richardson P.;  
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
 initiative";  
 RL Dev. Dyn. 225:384-391 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Ovary;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strassberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,  
 Raschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 Diatchenko L., Matusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stempleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Franke C.,  
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 Butlerfield Y.S.N., Krzywinski M.I., Skalski U., Smalins D.E.,  
 Schnerch A., Schein J.R., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Ovary;  
 RA Klein S., Gerhard D.S.;  
 RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC084288; AA84288.1; -; mRNA.  
 DR InterPro; IPR005647; Mdl1.  
 DR Pfam; PF03962; Mdl1; 1.  
 SQ SEQUENCE 205 AA; 24022 MW; 2EFE64865708262B CRC64;

Query Match 81.0%; Score 848; DB 2; Length 205;  
 Best Local Similarity 77.6%; Pred. No. 1.3e-44;  
 Matches 159; Conservative 27; Mismatches 19; Indels 0; Gaps 0;

QY 1 MSKKKGLSAEKRRTMMEIFSETKDVFPOLKDEKIAPEKGTITAMSVKVLQSLVDGMYD 60  
 DB 1 MSKKKGLSAEKRRTMMEIFSETKDVFPOLKDEKIAPEKGTITAMSVKVLQSLVDGMYD 60  
 QY 61 DCEIRIGTSNYWAFPSKALHARKHKLKLEVLISQLSGSGQSHASLOKSIKAKIGRCETERT 120  
 DB 61 DCEIRIGTSNYWAFPSKALHARKHKLKLEVLISQLSGSGQSHASLOKSIKAKIGRCETERT 120  
 QY 121 TRLAKESSLDQREQLAAVEKYKDCDPQVVEEIRQANKVAKAANRWTNIFAIKSWA 180  
 DB 121 TRLAKESSLDQREQLAAVEKYKDCDPQVVEEIRQANKVAKAANRWTNIFAIKSWA 180  
 QY 121 SKLVEELSLRHRKEELCADLEKCEKCDPVVEEIRQANKVAKADVNRWTNIFAIKSWA 180  
 DB 121 SKLVEELSLRHRKEELCADLEKCEKCDPVVEEIRQANKVAKADVNRWTNIFAIKSWA 180  
 QY 181 KRKGFEEKTIIDRTGIPEDFDYID 205  
 DB 181 KRKGFEEKTIIDRTGIPEDFDYID 205  
 QY 181 KKKFGFERQIDKNGILPEDFYID 205  
 DB 181 KKKFGFERQIDKNGILPEDFYID 205

RESULT 6  
 Q4SS06\_TETNG PRELIMINARY; PRT; 204 AA.  
 ID Q4SS06\_TETNG PRELIMINARY; PRT; 204 AA.  
 AC Q4SS06; PRT; 204 AA.

DT 13-SEP-2005 (Tremblrel. 31, Created)  
 DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)  
 DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)  
 DE Chromosome 18 SCAF1485, whole genome shotgun sequence.  
 DB (Fragment).  
 GN ORFNames=GSTENG0013672001;  
 OS Tetradodon nigroviridis (Green puffer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Tetradodon.  
 NCBI\_TaxId=99883;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
 Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
 Nicoud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
 Dastlva C., Salenouat M., Levy M., Boudet N., Castellano S.,  
 Anhouard C., Jubin C., Castell V., Katinka M., Vacherie B.,  
 Blomont C., Duprat S., Broctier P., Coutanceau J.P., Gouzy J.,  
 Parra G., Lardier G., Chapple C., McKernan K.J., McEwen P., Bosak S.,  
 Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,  
 Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
 Laudet V., Schachter V., Queller F., Saurin W., Searpelli C.,  
 Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;  
 RT "Genome duplication in the teleost fish Tetradodon nigroviridis reveals  
 the early vertebrate proto-karyotype";  
 RL Nature 431:946-957 (2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RG Genoscope; Whitehead Institute Centre for Genome Research;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 preliminary data.  
 DR EMBL; CA801014485; CAP96576.1; -; Genomic\_DNA.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 204 AA; 23844 MW; CAB21EFF264BA752 CRC64;

Query Match 74.8%; Score 783; DB 2; Length 204;  
 Best Local Similarity 72.1%; Pred. No. 1.3e-40;  
 Matches 147; Conservative 28; Mismatches 29; Indels 0; Gaps 0;

QY 2 SKKKGLSAEKRRTMMEIFSETKDVFPOLKDEKIAPEKGTITAMSVKVLQSLVDGMYD 61  
 DB 1 SKKKGLSAEKRRTMMEIFSETKDVFPOLKDEKIAPEKGTITAMSVKVLQSLVDGMYD 60  
 QY 62 CERIGTSNYWAFPSKALHARKHKLKLEVLISQLSGSGQSHASLOKSIKAKIGRCETERT 121  
 DB 61 CERIGTSNYWAFPSKALHARKHKLKLEVLISQLSGSGQSHASLOKSIKAKIGRCETERT 120  
 QY 122 RLAKELSLDQREQLAAVEKYKDCDPQVVEEIRQANKVAKAANRWTNIFAIKSWA 181  
 DB 122 RLAKELSLDQREQLAAVEKYKDCDPQVVEEIRQANKVAKAANRWTNIFAIKSWA 180  
 QY 121 SLKLELDLREERRLLAQLEKYKDCPEVVEEIRQANKVAKAANRWTNIFAIKSWA 180  
 DB 121 SLKLELDLREERRLLAQLEKYKDCPEVVEEIRQANKVAKAANRWTNIFAIKSWA 180  
 QY 182 KRKGFEEKTIIDRTGIPEDFDYID 205  
 DB 182 KRKGFEEKTIIDRTGIPEDFDYID 204  
 QY 181 KKKFGFERQIDKNGILPEDFYID 204  
 DB 181 KKKFGFERQIDKNGILPEDFYID 204

RESULT 7  
 Q6DC61\_BRARE PRELIMINARY; PRT; 220 AA.  
 ID Q6DC61\_BRARE PRELIMINARY; PRT; 220 AA.  
 AC Q6DC61; PRT; 220 AA.  
 DT 25-OCT-2004 (Tremblrel. 28, Created)  
 DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)  
 DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)  
 DE Zgc:101017.  
 GN ORFNames=zgc:101017;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxId=7955;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Singapore local strain, TISSUE=Embryo;  
 RX MEDLINE=22388257, PubMed=12477932, DOI=10.1073/pnae.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stepiencko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Roach S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Whaley J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywinski M.T., Skalska U., Smalins D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Singapore local strain, TISSUE=Embryo;  
 RA Director MGC Project;  
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC078223; AAH78223.1; -; mRNA.  
 DR ZFIN: ZDB-GENE-040801-116; zgc:101017.  
 DR InterPro: IPR005647; Mnd1.  
 DR Pfam: PF03962; Mnd1; 1.  
 SQ SEQUENCE 220 AA; 25176 MW; 90DEAA69311F4BF7 CRC64;

Query Match 61.5%; Score 644; DB 2; Length 220;  
 Best Local Similarity 71.8%; Pred. No. 4,8e-32;  
 Matches 125; Conservative 20; Mismatches 29; Indels 0; Gaps 0;

OY 1 MSKKKGLSAEKKRTMMEIFSETKDVPOLKLEKIAPEKGIITAMSVKVLQSLVDDGV 60  
 DB 1 MSKKKGLSLEKRSKMEIFETKOVFOLEKIAPEKGIITAMSVKVLQSLVDDGV 60  
 OY 61 DCEKIGTSNYWAFPSKALHARKHLEVLSESGSQKHA5LQKSIKAKIGRCETEER 120  
 DB 61 DTERVGTSNYWAFPSKALHARKHLEVLSESGSQKHA5LQKSIKAKIGRCETEER 120  
 OY 121 TRIAELSLDROEQKAEVVKYDCDPOVVEIRQANKVAKKANRTDNIIF 174  
 DB 121 EDLAKELTALQKQDQKVEIEKYQCDPAVVEIRNINAKVAKKANRTDNIIF 174  
 RESULT 8  
 OX NCBI\_TaxId=6182;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC MEDLINE=22879925, PubMed=12973349, DOI=10.1038/ng1336;  
 RX Hu W., Yan Q., Shen D.K., Liu F., Zhu Z.D., Song H.D., Xu X.R.,  
 RA Wang Z.J., Rong Y.P., Zeng L.C., Wu J., Zhang X., Wang J.J., Xu X.N.,  
 RA Wang S.Y., Fu G., Zhang X.L., Wang Z.Q., Brindley P.J., McManus D.P.,

RA Xue C.L., Feng Z., Chen Z., Han Z.G.;  
 RT "Evolutionary and biomedical implications of a Schistosoma japonicum  
 RT complementary DNA resource.";  
 RL Nat. Genet. 35:139-147(2003).  
 DR EMBL: AY223066; AAP06089.1; -; mRNA.  
 DR InterPro: IPR005647; Mnd1.  
 DR Pfam: PF03962; Mnd1; 1.  
 SQ SEQUENCE 196 AA; 23163 MW; B30F6F08BD7123F0 CRC64;

Query Match 44.1%; Score 462; DB 2; Length 196;  
 Best Local Similarity 47.4%; Pred. No. 6,4e-21;  
 Matches 92; Conservative 34; Mismatches 68; Indels 0; Gaps 0;

OY 11 EKRTMMEIFSETKDVPOLKLEKIAPEKGIITAMSVKVLQSLVDDGVDCERIGTSNY 70  
 DB 2 KSRQMDMPFEKKQDFOLKLEKIERLCQKEKIGINSVVDVLM5LHVDGIVDTDKIGTSY 61  
 OY 71 YWAFPSKALHARKHLEVLSESGSQKHA5LQKSIKAKIGRCETEERTLAELSL 130  
 DB 62 FWAFPSKAQKLRNNIEKVTGDIHTRQIQIFKTTSLNBLASKRQDTERRNIIINELTEL 121  
 OY 131 RDQREQLAEVVKYDCDPOVVEIRQANKVAKKANRTDNIIFAIKSWAKKFGFEERK 190  
 DB 122 KILLESLEAEQDLEKHPDRLELRQOQVAD5ANKRTDNIIFVIKSWLSNKFSLDEAT 181  
 OY 191 IDRTFGIPEDPDYI 204  
 DB 182 PCQGFEPENPDYI 195

RESULT 9  
 OX NCBI\_TaxId=294381;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=HM-1;IMSS;  
 RX PubMed=15729342, DOI=10.1038/nature03291.  
 RA Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,  
 RA Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.U., Nozaki T.,  
 RA Suh B., Pop M., Duchene M., Ackers J., Tammich E., Lejpe M.,  
 RA Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,  
 RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,  
 RA Jagers K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,  
 RA Quail M.A., Rabinowitz E., Noterczak H., Price C., Wang Z.,  
 RA Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Iohia A.,  
 RA Foster P.G., Sichteritz-Ponten T., Weber C., Singh U., Mukherjee C.,  
 RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,  
 RA Fraser C.M., Hall N.;  
 RT "The genome of the protist parasite Entamoeba histolytica.";  
 RL Nature 433:865-868(2005).  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL: AAFB01000572; EAL45733.1; -; Genomic\_DNA.  
 DR InterPro: IPR005647; Mnd1.  
 DR Pfam: PF03962; Mnd1; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 269 AA; 31920 MW; 63AD3885CF0387B3 CRC64;

Query Match 43.8%; Score 459; DB 2; Length 269;  
 Best Local Similarity 42.9%; Pred. No. 1,4e-20;  
 Matches 88; Conservative 53; Mismatches 64; Indels 0; Gaps 0;  
 OY 1 MSKKKGLSAEKKRTMMEIFSETKDVPOLKLEKIAPEKGIITAMSVKVLQSLVDDGV 60



[illegible]

Db 1 MSVSDVLMSTLVHGLVDVTDIGTSVYFWAPPSKAAQXLRNNIEKVTGDHIDTRNQIFKTT 60

Qy 105 KSLEKATIGCCFEEERRLRLKKEISLSDQEQBLKAEYKXKDCGPQVYEYSRQANKVAKE 164

Db 61 RSINEALSKKRDYEEERRRIINLEITELKILLESFLAEVLQDUEKHPDRLSERLQQLVALD 120

Qy 165 AANRWTDNIIFAIKSMWAKKFKCFEENKIDRTFGIPDEPDYI 204

Db 121 SANRWTDNIIFVIKSWLSNFSLDATCRQFEIPENDYI 160

RESULT 14

MCP7\_SCHPO

ID MCP7\_SCHPO STANDARD; PRT; 21.0 AA.

AC Q09739;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Meiotic coiled-coil protein 7.

GN Name=MCP7; ORFNames=SPAC13A11.03;

OS Schizosaccharomyces pombe (Fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomycetes.

OX NCBI\_TaxID=4896;

RN [1]

RP NUCLEOTIDE SEQUENCE, FUNCTION, AND INTERACTION WITH MEU13.

RA PubMed=15210864; DOI=10.1093/nar/gkh654;

RA Saito T.T., Tougan T., Kasama T., Okuzaki D., Nojima H.;

RT "MCP7, a meiosis-specific coiled-coil protein of fission yeast,

RL associates with Meu13 and is required for meiotic recombination.";

RL Nucleic Acids Res. 32:3325-3339(2004).

RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RA STRAIN=9712;

RC MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;

RX Wood V., Gwilliam R., Rajandream M.A., Lyne M.H., Lyne R., Stewart A.,

RA Sgouros J.G., Peat N., Hayles J., Baker S.G., Basham D., Bowman S.,

RA Brookes K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,

RA Gentles S., Goble A., Hamlin N., Harris D.B., Hidalgo J., Hodgson G.,

RA Holtroyd S., Hornsby T., Howarth S., Huckle E., Hunt S., Jagsels K.,

RA James K.D., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA Mooney P., Moutle S., Mungall K.L., Murphy L.D., Niblett D., Odell C.,

RA Oliver K., O'Neill S., Pearson D., Quail M.A., Raboinowitsch E.,

RA Rutherford K.M., Rutter S., Saunders D., Seeger K., Sharp S.,

RA Skelton J., Simmonds M.N., Squares R., Squares S., Stevens K.,

RA Taylor K., Taylor R.G., Tvey A., Walsh S.V., Warren T., Whitehead S.,

RA Woodward J.R., Volkert G., Aert R., Robben J., Grymponrez B.,

RA Weljans I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

RA Gabel C., Fuchs M., Duesterhoeft A., Fritz C., Holzer E., Moestl D.,

RA Hilbert H., Bozrym K., Langer I., Beck A., Lehnach H., Reinhardt R.,

RA Pohl T.M., Beger P., Zimmermann W., Wedler H., Wambut R., Purnelle B.,

RA Coffeau A., Cadieu E., Deyano S., Gloux S., Lelaure V., Mortier S.,

RA Galibert F., Aves S.J., Xiang Z., Hunt K., Moore K., Hurst S.M.,

RA Lucas M., Roche M., Gaillardin C., Talada V.A., Garzon A., Rhode G.,

RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,

RA Shipakovski G.V., Ussery D., Barrett B.G., Nurse P.;

RT "The genome sequence of *Schizosaccharomyces pombe*.";

RL Nature 415:871-880(2002).

CC -1- FUNCTION: Required for meiotic recombination.

CC -1- SUBUNIT: Interacts with meu13.

CC -1- -

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CC removed.

CC EMBL; AB189985; BAD24847.1; -; Genomic DNA.

CC EMBL; Z540966; CAA90804.1; -; Genomic DNA.

DR "PIR, T37610, T37610.  
DR GenedB Spombe; SPAC13A11.03; -.  
DR GO; GO:0000785; C:chromatin; IDA.  
DR GO; GO:0007131; P:meiotic recombination; IGI.  
DR GO; GO:0007129; P:synapsis; IMP.  
DR InterPro; IPR005647; Mnd1.  
DR Pfam; PF03962; Mnd1; 1.  
DR Coiled coil; Complete proteome; Melosia.  
FT COILED 77 148 Potential.  
SQ SEQUENCE 210 AA; 24224 MW; FA546F070A37665 CRC64;

Query Match 33.3%; Score 349; DB 1; Length 210;  
Best Local Similarity 41.6%; Pred. No. 6e-14;  
Matches 84; Conservative 36; Mismatches 76; Indels 6; Gaps 5;

QY 5 KGLAEEKRTMMEIFSETKDVOLKDEKIAPEKGITAMSVKEVLSLVDDGAVDCER 64  
DB 4 KGLSLAEKRRRLERLEIFHDSKDFOLKEVEKLGSK-KQIVLOTVDLQSLVDNIVKTEK 62  
QY 65 IGTSNYYWAPPSKALHARKHLEVLSEGSQKHSI--EKAKIGRCETE-BRT 121  
DB 63 IGTSNYYWSPSPDAKRSRESVLSLQQLDLDLKQSKTLDENISPEKSKRDNEGTEENDAN 122  
QY 122 RLAKELSLRP-QREQLKAEVEKYKDCDPQVEEIRQANKYAKAANRMTNIFAISMA 180  
DB 123 QYTELRLAKESLKLKTOLSNLNCNPETFEKNTKMYEAMLMTDQIHLLAFC 182  
QY 181 KRKFGFEENKIDRTFGIPEDFD 202  
DB 183 -RDMGADTNQIRYCSTPEDLD 203

## RESULT 15

Q8SUA9 ENCCU  
ID Q8SUA9 ENCCU PRELIMINARY; PRT; 203 AA.  
AC Q8SUA9  
DT 01-JUN-2002 (TREMBLrel. 21, Created)  
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Hypothetical protein ECU10.1600.  
GN OrderedLocustNames=ECU10.1600;  
OS Encephalitozoon cuniculi.  
OC Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.  
OX NCBI\_TaxId=6035;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=GB-M1;  
RX MEDLINE=21576510; PubMed=11719806; DOI=10.1038/35106579;  
RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,  
Prensler G., Barde V., Peyretailade E., Brottier P., Wincker P.,  
Dejbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,  
RA Weissenbach J., Vivares C.P.;  
RT "Genome sequence and gene compaction of the eukaryote parasite  
Encephalitozoon cuniculi.";  
RL Nature 414:450-453(2001).  
DR EMBL; AL590449; CAD25881.1; -; Genomic\_DNA.  
DR InterPro; IPR005647; Mnd1.  
DR Pfam; PF03962; Mnd1; 1.  
KM Complete proteome; Hypothetical protein.  
SQ SEQUENCE 203 AA; 23743 MW; DFE33A65A1A28A42 CRC64;

Query Match 32.5%; Score 340.5; DB 2; Length 203;  
Best Local Similarity 35.1%; Pred. No. 1.9e-13;  
Matches 71; Conservative 50; Mismatches 72; Indels 9; Gaps 3;

QY 7 LSAEBKRTMMEIFSETKDVOLKDEKIAPEKGITAMSVKEVLSLVDDGAVDCERIG 66  
DB 6 MKSDQKSLLEITIGSKSFFDLQELLESIGSK-KGIIVNTIKRIQQLVDDGLVYAEKVG 64  
QY 67 TSNYYWAPPSKALHARKHLEVLSEGSQKHSI--EKAKIGRCETEERTRLAKE 126  
DB 65 TSNLYWSPASRGIQKKDKURCKELMEECERMSQDICRKEVYINEMKSKHYTBERNLENK 124

QY 127 LSSL-----RQREQLKAEVEKYKDCDPQVEEIRQANKYAKAANRMTNIFAISMAKR 182  
DB 125 LNALMKIEQDQRE---ELGKFERTDPIAYDKLVAQRKENADECNRIIDNVFIIDYICS 180  
QY 183 KFGFEENKIDRTFGIPEDFDYI 204  
DB 181 KFGFEENKIDRTFGIPEDFDYI 202

Search completed: February 2, 2006, 12:51:01  
Job time : 122 secs



GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 2, 2006, 12:51:07 ; Search time 47 Seconds  
(without alignment)  
360.607 Million cell updates/sec

Title: US-10-087-190-3  
Perfect score: 1047  
Sequence: 1 MSKKKGSAEKKRTRMMEIF.....FEENKIDRTFGIPEDFDYID 205

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5 COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/6 COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/H COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/PCRTUS COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/RE COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfill1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1047	100.0	205	US-09-799-250B-2	Sequence 2, Appli
2	1011	96.6	198	US-09-799-250B-720	Sequence 720, App
3	948	90.5	205	US-09-799-250B-4	Sequence 4, Appli
4	593.5	56.7	127	US-09-621-976-4959	Sequence 4959, Ap
5	349	33.3	200	US-09-799-250B-5	Sequence 5, Appli
6	349	33.3	200	US-09-799-250B-721	Sequence 721, App
7	191.5	18.3	260	US-09-248-796A-14485	Sequence 14485, A
8	134.5	12.8	1270	US-09-538-092-1321	Sequence 1321, Ap
9	117	11.2	976	US-09-104-324B-4	Sequence 4, Appli
10	117	11.2	976	US-09-538-092-1339	Sequence 1339, Ap
11	114	10.9	284	US-09-914-259-55	Sequence 55, Appli
12	113.5	10.8	284	US-09-914-259-62	Sequence 62, Appli
13	112.5	10.7	630	US-09-248-796A-20275	Sequence 20275, A
14	112	10.7	284	US-09-914-259-43	Sequence 43, Appli
15	111	10.6	1937	US-09-538-092-918	Sequence 918, Appl
16	110	10.5	284	US-09-914-259-46	Sequence 46, Appli
17	110	10.5	284	US-09-914-259-49	Sequence 49, Appli
18	109.5	10.5	170	US-09-438-185A-708	Sequence 708, App
19	109.5	10.5	818	US-10-104-047-2546	Sequence 2546, Ap
20	109	10.4	284	US-09-914-259-51	Sequence 51, Appli
21	108.5	10.4	860	US-10-037-417-59	Sequence 59, Appli
22	108	10.3	817	US-09-248-796A-20276	Sequence 20276, A
23	107	10.2	281	US-09-914-259-63	Sequence 63, Appli
24	107	10.2	284	US-09-167-206-10	Sequence 10, Appli
25	107	10.2	284	US-09-914-259-40	Sequence 40, Appli
26	107	10.2	284	US-09-914-259-48	Sequence 48, Appli
27	107	10.2	284	US-09-914-259-50	Sequence 50, Appli

28	106.5	10.2	284	2	US-09-914-259-41	Sequence 41, Appli
29	106	10.1	243	2	US-10-104-047-3167	Sequence 3167, Ap
30	106	10.1	534	2	US-09-103-664A-2	Sequence 2, Appli
31	106	10.1	1786	2	US-08-973-462-8	Sequence 8, Appli
32	105.5	10.1	224	1	US-08-272-255-16	Sequence 16, Appli
33	105.5	10.1	224	4	PCT-US95-08565-16	Sequence 16, Appli
34	105.5	10.1	245	2	US-10-164-595-34	Sequence 34, Appli
35	105	10.0	245	2	US-09-914-259-65	Sequence 65, Appli
36	105	10.0	251	2	US-09-914-259-64	Sequence 64, Appli
37	105	10.0	284	2	US-09-914-259-60	Sequence 60, Appli
38	104	9.9	1939	2	US-09-538-092-915	Sequence 915, App
39	104	9.9	1939	2	US-09-949-016-11104	Sequence 11104, A
40	102	9.7	281	2	US-09-914-259-45	Sequence 45, Appli
41	102	9.7	284	2	US-09-914-259-47	Sequence 47, Appli
42	102	9.7	284	2	US-09-914-259-57	Sequence 57, Appli
43	102	9.7	372	1	US-07-813-584A-3	Sequence 3, Appli
44	102	9.7	372	1	US-08-330-515-3	Sequence 3, Appli
45	102	9.7	1031	2	US-09-914-259-24	Sequence 24, Appli

ALIGNMENTS

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RESULT 1
US-09-799-250B-2
; Sequence 2, Application US/09799250B
; Patent No. 6924358
; GENERAL INFORMATION:
; APPLICANT: Pia M. Challita-Bid
; APPLICANT: Rene S. Hubert
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Arthur B. Raitano
; APPLICANT: Mary Faris
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: H1PIF1: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.34US01 (511582003400)
; CURRENT APPLICATION NUMBER: US/09/799,250B
; CURRENT FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 721
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-250B-2
Query Match      100.0%; Score 1047; DB 2; Length 205;
Best Local Similarity 100.0%; Pred. No. 2.6e-94;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 MSKKKGSAEKKRTRMMEIFSETYDVFQKLEKIAPEKGIITAMSVKVLQSLYDDGAV 60
DB      1 MSKKKGSAEKKRTRMMEIFSETYDVFQKLEKIAPEKGIITAMSVKVLQSLYDDGAV 60
QY      1 MSKKKGSAEKKRTRMMEIFSETYDVFQKLEKIAPEKGIITAMSVKVLQSLYDDGAV 60
DB      1 MSKKKGSAEKKRTRMMEIFSETYDVFQKLEKIAPEKGIITAMSVKVLQSLYDDGAV 60
QY      61 DCEIRGINSNYWAPPSKALHARKKLTLYLESOLSSGSKHASLQKSIKAKIGRCETER 120
DB      61 DCEIRGINSNYWAPPSKALHARKKLTLYLESOLSSGSKHASLQKSIKAKIGRCETER 120
QY      121 TRIAKELSSLDQREQLKAEVEKYKDCPQVEVERIRQANKYAKKAEANMTDNIFAIKSWA 180
DB      121 TRIAKELSSLDQREQLKAEVEKYKDCPQVEVERIRQANKYAKKAEANMTDNIFAIKSWA 180
QY      181 KRKFGFEENKIDRTFGIPEDFDYID 205
DB      181 KRKFGFEENKIDRTFGIPEDFDYID 205
QY      181 KRKFGFEENKIDRTFGIPEDFDYID 205
DB      181 KRKFGFEENKIDRTFGIPEDFDYID 205
RESULT 2
US-09-799-250B-720
; Sequence 720, Application US/09799250B
; Patent No. 6924358
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TYPE: PRT  
ORGANISM: Schizosaccharomyces pombe  
US-09-799-2508-5

Query Match 33.3%; Score 349; DB 2; Length 200;  
Best Local Similarity 41.6%; Pred. No. 3.2e-26;  
Matches 84; Conservative 36; Mismatches 76; Indels 6; Gaps 5;

QY 5 KGLSABEKRRTMMEIFSETKDVFOLEKIAPEKKGITAMSVKEVLQSLVDGAVDCER 64  
DB 1 KGLSLAEKRRRLLEIFHDSKDFOLKEVEKLGSK-KQIVLOTVADLOSLVDNIVKTEK 59  
QY 65 IGTSNYYWAPPSKALHARKHLEVLSEQLSEGSQKHAISLOKSI--EKAKIGRCETE--ERT 121  
DB 60 IGTSNYYWSPSDAKRSRESYVLSLQAOQDLKOKSKTLDENISPEKSKRDNEGTENDAN 119  
QY 122 RLAEVLSLRD-QREQLKAEVEKTKDCDPQVEEIRQANKYAKAEANWTNIFAIKSWA 180  
DB 120 QYTFELHLAKESSEKLTQTOLSNLNHCNPETFEFLKNENTKXKMEANLMTDQIHLLAF 179  
QY 181 KRKGFEEENKIDRTFGIPEDFD 202  
DB 180 -RDMGADTNQIREYCSIPEDLD 200

RESULT 6  
US-09-799-2508-721  
Sequence 721, Application US/09799250B  
Patent No. 6924358  
GENERAL INFORMATION:  
APPLICANT: Rene S. Hubert  
APPLICANT: Pia M. Chailica-Bid  
APPLICANT: Steve Chappell Mitchell  
APPLICANT: Arthur B. Raitano  
APPLICANT: Mary Faris  
APPLICANT: Daniel E.H. Afar  
APPLICANT: Aya Jakobovics  
TITLE OF INVENTION: 121P1: A TISSUE SPECIFIC PROTEIN  
TITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCERS  
FILE REFERENCE: 129.340S01 (51582003400)  
CURRENT FILING DATE: 2003-07-14  
CURRENT APPLICATION NUMBER: US/09/799,250B  
NUMBER OF SEQ ID NOS: 721  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 721  
LENGTH: 200  
TYPE: PRT  
ORGANISM: Schizosaccharomyces pombe  
US-09-799-2508-721

Query Match 33.3%; Score 349; DB 2; Length 200;  
Best Local Similarity 41.6%; Pred. No. 3.2e-26;  
Matches 84; Conservative 36; Mismatches 76; Indels 6; Gaps 5;

QY 5 KGLSABEKRRTMMEIFSETKDVFOLEKIAPEKKGITAMSVKEVLQSLVDGAVDCER 64  
DB 1 KGLSLAEKRRRLLEIFHDSKDFOLKEVEKLGSK-KQIVLOTVADLOSLVDNIVKTEK 59  
QY 65 IGTSNYYWAPPSKALHARKHLEVLSEQLSEGSQKHAISLOKSI--EKAKIGRCETE--ERT 121  
DB 60 IGTSNYYWSPSDAKRSRESYVLSLQAOQDLKOKSKTLDENISPEKSKRDNEGTENDAN 119  
QY 122 RLAEVLSLRD-QREQLKAEVEKTKDCDPQVEEIRQANKYAKAEANWTNIFAIKSWA 180  
DB 120 QYTFELHLAKESSEKLTQTOLSNLNHCNPETFEFLKNENTKXKMEANLMTDQIHLLAF 179  
QY 181 KRKGFEEENKIDRTFGIPEDFD 202  
DB 180 -RDMGADTNQIREYCSIPEDLD 200

RESULT 7  
US-09-248-796A-14485

Sequence 14485, Application US/09248796A  
Patent No. 6747137  
GENERAL INFORMATION:

APPLICANT: Keith Weinstein et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
FILE REFERENCE: 107196.132  
CURRENT APPLICATION NUMBER: US/09/248,796A  
CURRENT FILING DATE: 1999-02-12  
PRIORITY APPLICATION NUMBER: US 60/074,725  
PRIORITY FILING DATE: 1998-02-13  
PRIORITY APPLICATION NUMBER: US 60/096,409  
PRIORITY FILING DATE: 1998-08-13  
NUMBER OF SEQ ID NOS: 28208  
SEQ ID NO 14485  
LENGTH: 260  
TYPE: PRT  
ORGANISM: Candida albicans  
US-09-248-796A-14485

Query Match 18.3%; Score 191.5; DB 2; Length 260;  
Best Local Similarity 27.1%; Pred. No. 1.1e-10;  
Matches 59; Conservative 47; Mismatches 75; Indels 37; Gaps 8;

QY 1 MSKKKGLSABEKRRTMMEIFSETKDVFOLEKIAPEKKGITAMSVKEVLQSLVDGAV 60  
DB 60 MPKKGLQGEKRLSALNWFQSDHMFYTLKEIESKSKCKIPWOMKELVLALVEGLV 119  
QY 61 DCEIGTSNYYWAPPSKALHARKHLEVLSEQLSEGSQKHAISLOKSIKAK-----IGR 114  
DB 120 EQRGCGTTLNLYWSP-----YLOHKKQ-----QETHRLNKTNTIANLETBDSLCR 165  
QY 115 C-FTEERTRLAKELSLR-----DREQLKAEVEKTKDCDPQVEEIRQANKYAKAEANA 166  
DB 166 CKDETGVNQTHERASAKTRFCDQSLERIDISQSLQSLKDSBS--VE-----NLVTSIAF 218  
QY 167 NRWTNIFAIKSWAKRKGFEEENKIDRTFGIPEDFDYI 204  
DB 219 --FSDSIDDIDICVLSRQGLTMTTLKTEFELPLEEERI 254

RESULT 8  
US-09-538-092-1321  
Sequence 1321, Application US/09538092  
Patent No. 6753314  
GENERAL INFORMATION:  
APPLICANT: Gloc, Loic  
APPLICANT: Mansfield, Traci A.  
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same  
FILE REFERENCE: 15966-542  
CURRENT APPLICATION NUMBER: US/09/538,092  
CURRENT FILING DATE: 2000-03-29  
PRIORITY APPLICATION NUMBER: 60/127,352  
PRIORITY FILING DATE: 1999-04-01  
PRIORITY APPLICATION NUMBER: 60/178,965  
PRIORITY FILING DATE: 2000-02-01  
NUMBER OF SEQ ID NOS: 1387  
SOFTWARE: CarafSeqFormatter Version 0.9  
SEQ ID NO 1321  
LENGTH: 1270  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc.feature  
LOCATION: (0)..(0)  
OTHER INFORMATION: Polypeptide Accession Number Q14203  
US-09-538-092-1321

Query Match 12.8%; Score 134.5; DB 2; Length 1270;  
Best Local Similarity 23.4%; Pred. No. 0.00032;  
Matches 50; Conservative 43; Mismatches 106; Indels 15; Gaps 5;

QY 2 SKKKGLSABEKRRTMMEIFSETKDVFOLEKIAPEKKGITAMSVKEVLQSLVDGAVD 61

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      271 ARKAKALEKERYMEMADTADALIEWATLDKMAEERAESLQOEVEALKERVDLTTD 330
      62 CER1-----GTSNYWAFPSKALHAR-KHKLVLBSQLSGSOQKASLQKSIKA 110
      331 LEIHKAEIEGSGAASSYOLKQLEBNALNALVNRMLSSSEKQEHYLOKMEK- 389
      111 KIGRCET--BERTRLANELSLRDQREQLKAEVEKYKDCDQVVEIRQANKVAKAANR 168
      390 KNGELVVRQQRERLQSELQAESESTIDELKEQVDAALGAE-EVEMLTDRMLNLEKVR 448
      169 WTDNIFAIKSAKKKPFEEKIKIDRTGIPEDFD 202
      449 LRETVDGLEANNENDELQENARETELELROLD 482

      Db
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      449 LRETVDGLEANNENDELQENARETELELROLD 482

      RESULT 9
      US-09-104-324B-4
      ; Sequence 4, Application US/09104324B
      ; Patent No. 6232460
      ; GENERAL INFORMATION:
      ; APPLICANT: T reed, Ozlem; Sahin, Ugur; Pfeundechuh, Michael
      ; TITLE OF INVENTION: Methods For Diagnosis And Treating Cancers.
      ; TITLE OF INVENTION: And Methods For Identifying Pathogenic Markers In A Sample Of
      ; NUMBER OF SEQUENCES: 4
      ; CORRESPONDENCE ADDRESSES:
      ; ADDRESS: Publight & Jaworski LLP
      ; STREET: 666 Fifth Avenue
      ; CITY: New York City
      ; STATE: New York
      ; ZIP: 10103
      ; COMPUTER READABLE FORM:
      ; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
      ; COMPUTER: IBM
      ; OPERATING SYSTEM: PC-DOS
      ; SOFTWARE: Wordperfect
      ; CURRENT APPLICATION DATA:
      ; APPLICATION NUMBER: US/09/104,324B
      ; FILING DATE: 25-June-1998
      ; CLASSIFICATION: 435
      ; PRIOR APPLICATION DATA:
      ; APPLICATION NUMBER: 08/892,702
      ; FILING DATE: 15-July-1997
      ; ATTORNEY/AGENT INFORMATION:
      ; NAME: Hanson, No. 623246oman D.
      ; REGISTRATION NUMBER: 30,946
      ; REFERENCE/DOCKET NUMBER: LUD 5491
      ; TELECOMMUNICATION INFORMATION:
      ; TELEPHONE: (212) 318-3000
      ; TELEFAX: (212) 752-5958
      ; INFORMATION FOR SEQ ID NO: 4:
      ; SEQUENCE CHARACTERISTICS:
      ; LENGTH: 976 amino acids
      ; TYPE: amino acid
      ; TOPOLOGY: linear
      ; US-09-104-324B-4

      Query Match 11.2%; Score 117; DB 2; Length 976;
      Best Local Similarity 23.9%; Pred. No. 0.012;
      Matches 63; Conservative 38; Mismatches 85; Indels 78; Gaps 13;

      3 KKKGLSAEE--KRRRMEI--FSETKDV-----FOLKLEKTLAPKEGITTAMSVKVL 51
      413 QKSSSELEMTKLTNNKVELEBKLVGEKETLLYENKQEKIABELKG--TEOELIGLL 471
      52 QSL---VDDGVNDCERIGTSNYWAFPSKAL-----HARKKLEVL- 90
      472 QAREKEVHDEIQTLAITTSQOYYSKEVKDLTELENKLNKTELTSHCNKLSLENKELT 531
      91 -----SOLSEGSQKASLQKSIKAKIGRCETEBRTRLAKELSLRDQREQ 136
      532 QETSDMTLELNKQOEDINNKKQOEBRMUKQIE--NLQETETQLRNELEYVREBELKQKDE 589

      Db
      532 QETSDMTLELNKQOEDINNKKQOEBRMUKQIE--NLQETETQLRNELEYVREBELKQKDE 589
      91 -----SOLSEGSQKASLQKSIKAKIGRCETEBRTRLAKELSLRDQREQ 136
      472 QAREKEVHDEIQTLAITTSQOYYSKEVKDLTELENKLNKTELTSHCNKLSLENKELT 531
      52 QSL---VDDGVNDCERIGTSNYWAFPSKAL-----HARKKLEVL- 90
      413 QKSSSELEMTKLTNNKVELEBKLVGEKETLLYENKQEKIABELKG--TEOELIGLL 471
      3 KKKGLSAEE--KRRRMEI--FSETKDV-----FOLKLEKTLAPKEGITTAMSVKVL 51

      RESULT 10
      US-09-538-092-1339
      ; Sequence 1339, Application US/09538092
      ; Patent No. 6753314
      ; GENERAL INFORMATION:
      ; APPLICANT: Gluc, Loic
      ; APPLICANT: Mansfield, Tracy A.
      ; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
      ; FILE REFERENCE: 15966-542
      ; CURRENT APPLICATION NUMBER: US/09/538,092
      ; PRIOR FILING DATE: 2000-03-29
      ; PRIOR APPLICATION NUMBER: 60/127,352
      ; PRIOR FILING DATE: 1999-04-01
      ; PRIOR APPLICATION NUMBER: 60/178,965
      ; PRIOR FILING DATE: 2000-02-01
      ; NUMBER OF SEQ ID NOS: 1387
      ; SOFTWARE: CurepatseqFormatter Version 0.9
      ; SEQ ID NO 1339
      ; LENGTH: 976
      ; TYPE: PRT
      ; ORGANISM: Homo sapiens
      ; FEATURE:
      ; NAME/KEY: misc_feature
      ; LOCATION: (0)..(0)
      ; OTHER INFORMATION: Polypeptide Accession Number Q15431
      ; US-09-538-092-1339

      Query Match 11.2%; Score 117; DB 2; Length 976;
      Best Local Similarity 23.9%; Pred. No. 0.012;
      Matches 63; Conservative 38; Mismatches 85; Indels 78; Gaps 13;

      3 KKKGLSAEE--KRRRMEI--FSETKDV-----FOLKLEKTLAPKEGITTAMSVKVL 51
      413 QKSSSELEMTKLTNNKVELEBKLVGEKETLLYENKQEKIABELKG--TEOELIGLL 471
      52 QSL---VDDGVNDCERIGTSNYWAFPSKAL-----HARKKLEVL- 90
      472 QAREKEVHDEIQTLAITTSQOYYSKEVKDLTELENKLNKTELTSHCNKLSLENKELT 531
      91 -----SOLSEGSQKASLQKSIKAKIGRCETEBRTRLAKELSLRDQREQ 136
      532 QETSDMTLELNKQOEDINNKKQOEBRMUKQIE--NLQETETQLRNELEYVREBELKQKDE 589
      137 LKAEVEKYKQ-CD-----POVVEIRQANKVAKA--AANRWDNIFAIK----- 177
      590 VKCKLDKSEBNCNNLRQVENKKNYIELOQENRALKKGGTAESKOLNVAEIKVKNKLELE 649
      178 -SWAKRFG-----FEEENKI 191
      650 LESAKQKFGSEITDTTYQKEIEDKKI 673

      Db
      650 LESAKQKFGSEITDTTYQKEIEDKKI 673
      178 -SWAKRFG-----FEEENKI 191
      590 VKCKLDKSEBNCNNLRQVENKKNYIELOQENRALKKGGTAESKOLNVAEIKVKNKLELE 649
      137 LKAEVEKYKQ-CD-----POVVEIRQANKVAKA--AANRWDNIFAIK----- 177
      532 QETSDMTLELNKQOEDINNKKQOEBRMUKQIE--NLQETETQLRNELEYVREBELKQKDE 589
      413 QKSSSELEMTKLTNNKVELEBKLVGEKETLLYENKQEKIABELKG--TEOELIGLL 471
      3 KKKGLSAEE--KRRRMEI--FSETKDV-----FOLKLEKTLAPKEGITTAMSVKVL 51

      RESULT 11
      US-09-914-259-55
      ; Sequence 55, Application US/09914259
      ; Patent No. 6495336
      ; GENERAL INFORMATION:
      ; APPLICANT: Makowski, Lee
      ; APPLICANT: Hyman, Paul
      ; APPLICANT: Williams, Mark
      ; TITLE OF INVENTION: STRAGED ASSEMBLY OF NANOSTRUCTURES
      ; FILE REFERENCE: 8471-010-999
      ; CURRENT APPLICATION NUMBER: US/09/914,259
```

```

      137 LKAEVEKYKQ-CD-----POVVEIRQANKVAKA--AANRWDNIFAIK----- 177
      590 VKCKLDKSEBNCNNLRQVENKKNYIELOQENRALKKGGTAESKOLNVAEIKVKNKLELE 649
      178 -SWAKRFG-----FEEENKI 191
      650 LESAKQKFGSEITDTTYQKEIEDKKI 673

      Db
      650 LESAKQKFGSEITDTTYQKEIEDKKI 673
      178 -SWAKRFG-----FEEENKI 191
      590 VKCKLDKSEBNCNNLRQVENKKNYIELOQENRALKKGGTAESKOLNVAEIKVKNKLELE 649
      137 LKAEVEKYKQ-CD-----POVVEIRQANKVAKA--AANRWDNIFAIK----- 177
      532 QETSDMTLELNKQOEDINNKKQOEBRMUKQIE--NLQETETQLRNELEYVREBELKQKDE 589
      413 QKSSSELEMTKLTNNKVELEBKLVGEKETLLYENKQEKIABELKG--TEOELIGLL 471
      3 KKKGLSAEE--KRRRMEI--FSETKDV-----FOLKLEKTLAPKEGITTAMSVKVL 51

      RESULT 11
      US-09-914-259-55
      ; Sequence 55, Application US/09914259
      ; Patent No. 6495336
      ; GENERAL INFORMATION:
      ; APPLICANT: Makowski, Lee
      ; APPLICANT: Hyman, Paul
      ; APPLICANT: Williams, Mark
      ; TITLE OF INVENTION: STRAGED ASSEMBLY OF NANOSTRUCTURES
      ; FILE REFERENCE: 8471-010-999
      ; CURRENT APPLICATION NUMBER: US/09/914,259
```

;; CURRENT FILING DATE: 2000-11-21  
;; NUMBER OF SEQ ID NOS: 180  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 55  
;; LENGTH: 284  
;; TYPE: PRT  
;; ORGANISM: Sus scrofa  
US-09-914-259-55

Query Match 10.9%; Score 114; DB 2; Length 284;  
Best Local Similarity 23.2%; Pred. No. 0.0043;  
Matches 52; Conservative 37; Mismatches 61; Indels 74; Gaps 11;

Qy 1 MSKKKGLSAE---EKRTTMEIFSETKDVFOQLKLEKIAPEKKGITAMSVKEVQLSLVD 57  
Db 73 LAEKATDADAEADVASLNRRIOQLFEEELDRAQ-----ERLA-----TALQKLEAKADE 122  
Qy 58 ---GMVDCERIGTSNYWAPPSKALHAR---KHKLEVLSEQLSEGSQK----- 100  
Db 123 SERGM-----KYLESPAQDSEKMEIOETQLKEA--KHAEDADRYE 163  
Qy 101 -----ASLOKSEKAKI--GRCTEERTRLAKELSLDRQELKAEVEKYKCD 148  
Db 164 EVARKLVIESDLEPAERAEISBGK-----ALIEBELKTVTNKLKLEAQAEKYSQKE 218  
Qy 149 PQVVEIRQANKVAKEANRWTDNIFAIKSWAKRKGFEEENKID 192  
Db 219 DKYEIEIKVLSDKLKEAFTR-----AFAERSVTLKESID 254

RESULT 12  
US-09-914-259-62  
;; Sequence 62, Application US/09914259  
;; Patent No. 6495336  
;; GENERAL INFORMATION:  
;; APPLICANT: Makowski, Lee  
;; APPLICANT: Hyman, Paul  
;; APPLICANT: Williams, Mark  
;; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES  
;; FILE REFERENCE: 8471-010-999  
;; CURRENT APPLICATION NUMBER: US/09/914,259  
;; CURRENT FILING DATE: 2000-11-21  
;; NUMBER OF SEQ ID NOS: 180  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 62  
;; LENGTH: 284  
;; TYPE: PRT  
;; ORGANISM: Rattus norvegicus  
US-09-914-259-62

Query Match 10.8%; Score 113.5; DB 2; Length 284;  
Best Local Similarity 21.1%; Pred. No. 0.0048;  
Matches 48; Conservative 48; Mismatches 78; Indels 53; Gaps 8;

Qy 2 SKKKGLSA-EKRTTMEIFSETKDVFOQLKLEKIAPEKKGITAMSVK-EVQLSLVDGM 59  
Db 45 AKETLIRASEBRDVRVLELHKAEDSLAAD-ETPAKAEADVASLNRRIOQLVEEELDRAQ 103  
Qy 60 VDCERIGTSNYWAPPSKALHARKHLEVLSEQLSEGSQK----- 99  
Db 104 ---ERLATATQKLEBAEKAADESEGMKVISSRAQKDEKMEIOETQLKEAKHIAEDADR 160  
Qy 100 -----HASLOKSEKAKI--GRCTEERTRLAKELSLDRQELKAEVEKYK 145  
Db 161 KYEEVARLVIESDLEPAERAEISBGK-----ALIEBELKTVTNKLKLEAQAEKYS 215  
Qy 146 DCDPQVVEIRQANKVAKEANRWTDNIFAIKSWAKRKGFEEENKID 192  
Db 216 QKEKYEIEIKVLSDKLKEAFTR-----AFAERSVTLKESID 254

RESULT 13  
US-09-248-796A-20275

;; Sequence 20275, Application US/09248796A

;; Patent No. 6747137  
;; GENERAL INFORMATION:  
;; APPLICANT: Keith Weinstein et al  
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS  
;; FILE REFERENCE: 107196.132  
;; CURRENT APPLICATION NUMBER: US/09/248,796A  
;; CURRENT FILING DATE: 1999-02-12  
;; PRIOR APPLICATION NUMBER: US 60/074,725  
;; PRIOR FILING DATE: 1998-02-13  
;; PRIOR APPLICATION NUMBER: US 60/096,409  
;; PRIOR FILING DATE: 1998-08-13  
;; NUMBER OF SEQ ID NOS: 28208  
;; SEQ ID NO 20275  
;; LENGTH: 630  
;; TYPE: PRT  
;; ORGANISM: Candida albicans  
US-09-248-796A-20275

Query Match 10.7%; Score 112.5; DB 2; Length 630;  
Best Local Similarity 23.8%; Pred. No. 0.018;  
Matches 49; Conservative 43; Mismatches 79; Indels 35; Gaps 8;

Qy 3 KKKGLSAEKKRTTMEIFSETKDVFOQLKLEKIAPEKKGIT-AMSVKEVQLSLVDGMV 60  
Db 158 KTKNSDTELKLEKLELEKVK-----LDLQADEKLGITERIALKSELETVNKSG-- 210  
Qy 61 DCEIGTSNYWAPPS--KALHARKHLEVL-----ESQLSEGSQKHAASLOKSI----- 107  
Db 211 ---LSTTSELAAULTKTVKSLKEKEKELOFLSGNKSKELEDTIQHSDISEKLTBL 266  
Qy 108 -EKAKIGRCTEERTRLAKELSLDRQELKAEVEKYKCDPQVVEIRQANKVAKEAA 166  
Db 267 KEKTKQPDSSKKGLTELENDLTSTKEIETKTSKRNLEBRDKXIVLKNLELLK 326  
Qy 167 NRWTDNIFAIKSWAKRKGFEEENKID 192  
Db 327 N---DN-----SGAKKLEIKVSKLE 344

RESULT 14  
US-09-914-259-43  
;; Sequence 43, Application US/09914259  
;; Patent No. 6495336  
;; GENERAL INFORMATION:  
;; APPLICANT: Makowski, Lee  
;; APPLICANT: Hyman, Paul  
;; APPLICANT: Williams, Mark  
;; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES  
;; FILE REFERENCE: 8471-010-999  
;; CURRENT APPLICATION NUMBER: US/09/914,259  
;; CURRENT FILING DATE: 2000-11-21  
;; NUMBER OF SEQ ID NOS: 180  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 43  
;; LENGTH: 284  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-914-259-43

Query Match 10.7%; Score 112; DB 2; Length 284;  
Best Local Similarity 23.5%; Pred. No. 0.0068;  
Matches 52; Conservative 41; Mismatches 72; Indels 56; Gaps 9;

Qy 1 MSKKKGLSAEEK---RTTMEIFSETKDVFO-----LKDEKIAPK-EKGITAMSV 47  
Db 73 LAEKKAADAEADVASLNRRIOQLVEEELDRAQERLATATQKLEBAEKAADESEGMKVIEN 132  
Qy 48 KEVQLSLVDGMVDCERIGTSNYWAPPSKALHARKHLEVLSEQLSEGSQKHAASLOKSI 107  
Db 133 R---ALKDEKMEIOET-----OLKEAKHIAEDADRYEEVARLVIEBDL 176

[illegible]

## RESULT 15

```

US-09-538-092-918
; Sequence 918: Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratPseqFormatter Version 0.9
; SEQ ID NO 918
; LENGTH: 1937
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)_(0)
; OTHER INFORMATION: Polypeptide Accession Number P13535
US-09-538-092-918

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Query match	10.64;	Score 111;	DB 2;	Length 1937;
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Matches 54; Conservative 42; Mismatches 88; Indels 50; Gaps 9;

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OY      4 KKGJSAEKRFRMMMEI FSEETKDFVQFKLEKIAPK-----EKGITRMS-----V 47
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1361 QPALSKANSEVAQWRTKYTEIDALIQTEBELSEKKKLQALRQCEAEHVAANNAKCSLEKT 14220
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      48 KEVIOSLVDGCVDCERIGTS-----NYMAFPAKALHARKHKEVLSESQISEGQ 98
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1421 KQRLQNEVEDLMDLVYERSNAAALDQKQRNF-----DKVISEWQKYTEBQALIELASQ 1475
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      99 KHASIQKSIIEKAK-----IGRCET--EERTPLAKELSSLRQ-----RQQLKAE 140
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1476 ESRSLSTELFKVKONYEESLDQLETLERENKULOEOEIDLTQIQAEGGKOIHELEKIKQ 1535
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      141 VEKYUDCPQVVEEIRQANKYAKA--ANRWTDNIIAITSMAKRGKGFENKIDR 193
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1536 VEQEK--CEIQAALEAEASLEHESKIKIRIQLELQOVSEVDRIKAEDEBIDQ 1568
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Search completed: February 2, 2006, 12:52:34  
Job time : 48 secs





GENERAL INFORMATION:  
APPLICANT: Agensys, Inc.  
APPLICANT: Chailita-Bid, Pia M.  
APPLICANT: Hubbert, Rene S.  
APPLICANT: Raitano, Arthur B.  
APPLICANT: Faris, Mary  
APPLICANT: Afar, Daniel E. H.  
APPLICANT: Ge, Mangmao  
APPLICANT: Jakobovitz, Aya  
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN  
FILE REFERENCE: 51158-20034.20  
CURRENT FILING DATE: 2003-01-28  
PRIOR APPLICATION NUMBER: US 09/779,250  
NUMBER OF SEQ ID NOS: 69  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 205  
TYPE: PRT  
ORGANISM: Homo Sapiens  
US-10-087-190-3

Query Match 100.0%; Score 1047; DB 4; Length 205;  
Best Local Similarity 100.0%; Pred. No. 4e-78;  
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MSKKGSAEKKRRMEIFSETKDVOLKLEKIAPEKIGITAMSVKVEVLSVDDGMV 60  
DB 1 MSKKGSAEKKRRMEIFSETKDVOLKLEKIAPEKIGITAMSVKVEVLSVDDGMV 60  
QY 61 DCEIGTSNYWAPPSKALHARKHKLTVLSQSLSEGSQKASLSQKSIKAKIGRCETEE 120  
DB 61 DCEIGTSNYWAPPSKALHARKHKLTVLSQSLSEGSQKASLSQKSIKAKIGRCETEE 120  
QY 121 TRAKELSSLRDQEQKAEVEKYKDCDPVVEEIRQANKVAKAANRWTDNIFAISWA 180  
DB 121 TRAKELSSLRDQEQKAEVEKYKDCDPVVEEIRQANKVAKAANRWTDNIFAISWA 180  
QY 181 KRKGFENKIDRTFGIPEDFDYID 205  
DB 181 KRKGFENKIDRTFGIPEDFDYID 205

RESULT 3  
US-10-087-190-14  
Sequence 14, Application US/10087190  
Publication No. US2003022397A1  
GENERAL INFORMATION:  
APPLICANT: Agensys, Inc.  
APPLICANT: Chailita-Bid, Pia M.  
APPLICANT: Hubbert, Rene S.  
APPLICANT: Raitano, Arthur B.  
APPLICANT: Faris, Mary  
APPLICANT: Afar, Daniel E. H.  
APPLICANT: Ge, Mangmao  
APPLICANT: Jakobovitz, Aya  
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN  
FILE REFERENCE: 51158-20034.20  
CURRENT FILING DATE: 2003-01-28  
PRIOR APPLICATION NUMBER: US 09/779,250  
NUMBER OF SEQ ID NOS: 69  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 14  
LENGTH: 205  
TYPE: PRT  
ORGANISM: Homo Sapiens  
US-10-087-190-14

Query Match 100.0%; Score 1047; DB 4; Length 205;  
Best Local Similarity 100.0%; Pred. No. 4e-78;  
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MSKKGSAEKKRRMEIFSETKDVOLKLEKIAPEKIGITAMSVKVEVLSVDDGMV 60  
DB 1 MSKKGSAEKKRRMEIFSETKDVOLKLEKIAPEKIGITAMSVKVEVLSVDDGMV 60  
QY 61 DCEIGTSNYWAPPSKALHARKHKLTVLSQSLSEGSQKASLSQKSIKAKIGRCETEE 120  
DB 61 DCEIGTSNYWAPPSKALHARKHKLTVLSQSLSEGSQKASLSQKSIKAKIGRCETEE 120  
QY 121 TRAKELSSLRDQEQKAEVEKYKDCDPVVEEIRQANKVAKAANRWTDNIFAISWA 180  
DB 121 TRAKELSSLRDQEQKAEVEKYKDCDPVVEEIRQANKVAKAANRWTDNIFAISWA 180  
QY 181 KRKGFENKIDRTFGIPEDFDYID 205  
DB 181 KRKGFENKIDRTFGIPEDFDYID 205

RESULT 4  
US-10-087-190-20  
Sequence 20, Application US/10087190  
Publication No. US2003022397A1  
GENERAL INFORMATION:  
APPLICANT: Agensys, Inc.  
APPLICANT: Chailita-Bid, Pia M.  
APPLICANT: Hubbert, Rene S.  
APPLICANT: Raitano, Arthur B.  
APPLICANT: Faris, Mary  
APPLICANT: Afar, Daniel E. H.  
APPLICANT: Ge, Mangmao  
APPLICANT: Jakobovitz, Aya  
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN  
FILE REFERENCE: 51158-20034.20  
CURRENT FILING DATE: 2003-01-28  
PRIOR APPLICATION NUMBER: US 09/779,250  
NUMBER OF SEQ ID NOS: 69  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 20  
LENGTH: 205  
TYPE: PRT  
ORGANISM: Homo Sapiens  
US-10-087-190-20

Query Match 100.0%; Score 1047; DB 4; Length 205;  
Best Local Similarity 100.0%; Pred. No. 4e-78;  
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MSKKGSAEKKRRMEIFSETKDVOLKLEKIAPEKIGITAMSVKVEVLSVDDGMV 60  
DB 1 MSKKGSAEKKRRMEIFSETKDVOLKLEKIAPEKIGITAMSVKVEVLSVDDGMV 60  
QY 61 DCEIGTSNYWAPPSKALHARKHKLTVLSQSLSEGSQKASLSQKSIKAKIGRCETEE 120  
DB 61 DCEIGTSNYWAPPSKALHARKHKLTVLSQSLSEGSQKASLSQKSIKAKIGRCETEE 120  
QY 121 TRAKELSSLRDQEQKAEVEKYKDCDPVVEEIRQANKVAKAANRWTDNIFAISWA 180  
DB 121 TRAKELSSLRDQEQKAEVEKYKDCDPVVEEIRQANKVAKAANRWTDNIFAISWA 180  
QY 181 KRKGFENKIDRTFGIPEDFDYID 205  
DB 181 KRKGFENKIDRTFGIPEDFDYID 205

RESULT 5  
US-10-087-190-21  
Sequence 21, Application US/10087190

```
Publication No. US2003022397A1
GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
APPLICANT: Chailita-Bid, Pia M.
APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur B.
APPLICANT: Paris, Mary
APPLICANT: Afar, Daniel E. H.
APPLICANT: Ge, Mangmao
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P1 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20034.20
CURRENT APPLICATION NUMBER: US/10/087,190
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 205
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-087-190-21

Query Match          100.0%; Score 1047; DB 4; Length 205;
Best Local Similarity 100.0%; Pred. No. 4e-78;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSKKKGSAEKKRTTRMEIFSETKDVFLKDLKIAPEKIGITMSVKEVLSLVDDGMV 60
DB 1 MSKKKGSAEKKRTTRMEIFSETKDVFLKDLKIAPEKIGITMSVKEVLSLVDDGMV 60
QY 61 DCEIGTSNYWAPPSPKALHARKKLEVLSEQLSEGSQKASLQKSIKAKIGRCETEE 120
DB 61 DCEIGTSNYWAPPSPKALHARKKLEVLSEQLSEGSQKASLQKSIKAKIGRCETEE 120
QY 121 TRLAKELSLDQREQLKAEVEKYKDCDPQVEEIRQANKVAKAANWTNIFAISMA 180
DB 121 TRLAKELSLDQREQLKAEVEKYKDCDPQVEEIRQANKVAKAANWTNIFAISMA 180
QY 181 KRKGFPEENKIDRTFGIPEDFYID 205
DB 181 KRKGFPEENKIDRTFGIPEDFYID 205

RESULT 6
US-10-087-190-22
Sequence 22, Application US/10087190
Publication No. US2003022397A1
GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
APPLICANT: Chailita-Bid, Pia M.
APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur B.
APPLICANT: Paris, Mary
APPLICANT: Afar, Daniel E. H.
APPLICANT: Ge, Mangmao
APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P1 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20034.20
CURRENT APPLICATION NUMBER: US/10/087,190
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 205
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-087-190-22
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Query Match          100.0%; Score 1047; DB 4; Length 205;
Best Local Similarity 100.0%; Pred. No. 4e-78;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSKKKGSAEKKRTTRMEIFSETKDVFLKDLKIAPEKIGITMSVKEVLSLVDDGMV 60
DB 1 MSKKKGSAEKKRTTRMEIFSETKDVFLKDLKIAPEKIGITMSVKEVLSLVDDGMV 60
QY 61 DCEIGTSNYWAPPSPKALHARKKLEVLSEQLSEGSQKASLQKSIKAKIGRCETEE 120
DB 61 DCEIGTSNYWAPPSPKALHARKKLEVLSEQLSEGSQKASLQKSIKAKIGRCETEE 120
QY 121 TRLAKELSLDQREQLKAEVEKYKDCDPQVEEIRQANKVAKAANWTNIFAISMA 180
DB 121 TRLAKELSLDQREQLKAEVEKYKDCDPQVEEIRQANKVAKAANWTNIFAISMA 180
QY 181 KRKGFPEENKIDRTFGIPEDFYID 205
DB 181 KRKGFPEENKIDRTFGIPEDFYID 205

RESULT 7
US-10-087-190-61
Sequence 61, Application US/10087190
Publication No. US2003022397A1
GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
APPLICANT: Chailita-Bid, Pia M.
APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur B.
APPLICANT: Paris, Mary
APPLICANT: Afar, Daniel E. H.
APPLICANT: Ge, Mangmao
APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P1 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20034.20
CURRENT APPLICATION NUMBER: US/10/087,190
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 61
LENGTH: 205
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-087-190-61

Query Match          100.0%; Score 1047; DB 4; Length 205;
Best Local Similarity 100.0%; Pred. No. 4e-78;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSKKKGSAEKKRTTRMEIFSETKDVFLKDLKIAPEKIGITMSVKEVLSLVDDGMV 60
DB 1 MSKKKGSAEKKRTTRMEIFSETKDVFLKDLKIAPEKIGITMSVKEVLSLVDDGMV 60
QY 61 DCEIGTSNYWAPPSPKALHARKKLEVLSEQLSEGSQKASLQKSIKAKIGRCETEE 120
DB 61 DCEIGTSNYWAPPSPKALHARKKLEVLSEQLSEGSQKASLQKSIKAKIGRCETEE 120
QY 121 TRLAKELSLDQREQLKAEVEKYKDCDPQVEEIRQANKVAKAANWTNIFAISMA 180
DB 121 TRLAKELSLDQREQLKAEVEKYKDCDPQVEEIRQANKVAKAANWTNIFAISMA 180
QY 181 KRKGFPEENKIDRTFGIPEDFYID 205
DB 181 KRKGFPEENKIDRTFGIPEDFYID 205

RESULT 8
US-10-408-765A-1821
```

; Sequence 1821, Application US/10408765A  
; Publication No. US20040101874A1  
; GENERAL INFORMATION:  
; APPLICANT: Ghosh, Soumitra S.  
; APPLICANT: Baby, Eoin D.  
; APPLICANT: Zhang, Bing  
; APPLICANT: Gibson, Bradford W.  
; APPLICANT: Taylor, Steven W.  
; APPLICANT: Glenn, Gary M.  
; APPLICANT: Marnock, Dale E.  
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME  
; FILE REFERENCE: 660088.465  
; CURRENT APPLICATION NUMBER: US/10/408,765A  
; CURRENT FILING DATE: 2003-04-04  
; NUMBER OF SEQ ID NOS: 3077  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1821  
; LENGTH: 205  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-408-765A-1821

Query Match 100.0%; Score 1047; DB 4; Length 205;  
Best Local Similarity 100.0%; Pred. No. 4e-78;  
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSKKKGSAEKKRTMMEIFSETKQVDFQKDLKIAPEKIGITAMSVKVLQSLVDDGMV 60  
1 MSKKKGSAEKKRTMMEIFSETKQVDFQKDLKIAPEKIGITAMSVKVLQSLVDDGMV 60  
Db 1 MSKKKGSAEKKRTMMEIFSETKQVDFQKDLKIAPEKIGITAMSVKVLQSLVDDGMV 60  
Qy 61 DCEIRIGTSNYWAPPSKALHARKHKLTVLSQSLSGSQKHA5LOKSIKAKIGRCETEE 120  
Db 61 DCEIRIGTSNYWAPPSKALHARKHKLTVLSQSLSGSQKHA5LOKSIKAKIGRCETEE 120  
Qy 121 TRLAKEISSLRDQREQLKAEVEKYKDCDPQVVEIRQANKVAKAANRWTDNIPAIKSWA 180  
Db 121 TRLAKEISSLRDQREQLKAEVEKYKDCDPQVVEIRQANKVAKAANRWTDNIPAIKSWA 180  
Qy 181 KRKGFEEKNKIDRTFGIPEDFDYID 205  
Db 181 KRKGFEEKNKIDRTFGIPEDFDYID 205

RESULT 9  
US-11-125-805-2  
; Sequence 2, Application US/11125805  
; Publication No. US20050208059A1  
; GENERAL INFORMATION:  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Pia M. Challita-Bid  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Mary Faris  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Aya Jakobovitz  
; TITLE OF INVENTION: 121P1: A TISSUE SPECIFIC PROTEIN  
; TITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCERS  
; FILE REFERENCE: 129.34US01 (511582003400)  
; CURRENT APPLICATION NUMBER: US/11/125,805  
; CURRENT FILING DATE: 2005-05-09  
; PRIOR APPLICATION NUMBER: US/09/799,250B  
; NUMBER OF SEQ ID NOS: 721  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 205  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-125-805-2

Query Match 100.0%; Score 1047; DB 6; Length 205;  
Best Local Similarity 100.0%; Pred. No. 4e-78;

Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MSKKKGSAEKKRTMMEIFSETKQVDFQKDLKIAPEKIGITAMSVKVLQSLVDDGMV 60  
1 MSKKKGSAEKKRTMMEIFSETKQVDFQKDLKIAPEKIGITAMSVKVLQSLVDDGMV 60  
Db 1 MSKKKGSAEKKRTMMEIFSETKQVDFQKDLKIAPEKIGITAMSVKVLQSLVDDGMV 60  
Qy 61 DCEIRIGTSNYWAPPSKALHARKHKLTVLSQSLSGSQKHA5LOKSIKAKIGRCETEE 120  
Db 61 DCEIRIGTSNYWAPPSKALHARKHKLTVLSQSLSGSQKHA5LOKSIKAKIGRCETEE 120  
Qy 121 TRLAKEISSLRDQREQLKAEVEKYKDCDPQVVEIRQANKVAKAANRWTDNIPAIKSWA 180  
Db 121 TRLAKEISSLRDQREQLKAEVEKYKDCDPQVVEIRQANKVAKAANRWTDNIPAIKSWA 180  
Qy 181 KRKGFEEKNKIDRTFGIPEDFDYID 205  
Db 181 KRKGFEEKNKIDRTFGIPEDFDYID 205

RESULT 10  
US-10-087-190-44  
; Sequence 44, Application US/10087190  
; Publication No. US20030223977A1  
; GENERAL INFORMATION:  
; APPLICANT: Agensys, Inc.  
; APPLICANT: Challita-Bid, Pia M.  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Faris, Mary  
; APPLICANT: Afar, Daniel E. H.  
; APPLICANT: Ge, Mangiao  
; APPLICANT: Jakobovitz, Aya  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN  
; FILE REFERENCE: 51158-20034.20  
; CURRENT APPLICATION NUMBER: US/10/087,190  
; CURRENT FILING DATE: 2003-01-28  
; PRIOR APPLICATION NUMBER: US 09/779,250  
; PRIOR FILING DATE: 2001-03-05  
; NUMBER OF SEQ ID NOS: 69  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 44  
; LENGTH: 206  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-087-190-44

Query Match 99.0%; Score 1036.5; DB 4; Length 206;  
Best Local Similarity 99.5%; Pred. No. 3e-77;  
Matches 205; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MSKKKGSAEKKRTMMEIFSETKQVDFQKDLKIAPEKIGITAMSVKVLQSLVDDGMV 60  
1 MSKKKGSAEKKRTMMEIFSETKQVDFQKDLKIAPEKIGITAMSVKVLQSLVDDGMV 60  
Db 1 MSKKKGSAEKKRTMMEIFSETKQVDFQKDLKIAPEKIGITAMSVKVLQSLVDDGMV 60  
Qy 61 DCEIRIGTSNYWAPPSKALHARKHKLTVLSQSLSGSQKHA5LOKSIKAKIGRCETEE 119  
Db 61 DCEIRIGTSNYWAPPSKALHARKHKLTVLSQSLSGSQKHA5LOKSIKAKIGRCETEE 120  
Qy 120 RTRLAKEISSLRDQREQLKAEVEKYKDCDPQVVEIRQANKVAKAANRWTDNIPAIKSW 179  
Db 120 RTRLAKEISSLRDQREQLKAEVEKYKDCDPQVVEIRQANKVAKAANRWTDNIPAIKSW 180  
Qy 180 KRKGFEEKNKIDRTFGIPEDFDYID 205  
Db 180 KRKGFEEKNKIDRTFGIPEDFDYID 206

RESULT 11  
US-10-087-190-45  
; Sequence 45, Application US/10087190  
; Publication No. US20030223977A1  
; GENERAL INFORMATION:

APPLICANT: Agensys, Inc.  
APPLICANT: Challita-Bid, Pia M.  
APPLICANT: Hubert, Rene S.  
APPLICANT: Raitano, Arthur B.  
APPLICANT: Farris, Mary  
APPLICANT: Afari, Daniel E. H.  
APPLICANT: Ge, Wangmao  
APPLICANT: Jakobovits, Aya  
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN  
TITLE OF INVENTION: ENTITLED 121P11 USERFUL IN TREATMENT AND DETECTION OF CANCER  
FILE REFERENCE: 51158-20034.20  
CURRENT APPLICATION NUMBER: US/10/087.190  
CURRENT FILING DATE: 2003-01-28  
PRIOR APPLICATION NUMBER: US 09/779,250  
PRIOR FILING DATE: 2001-03-05  
NUMBER OF SEQ ID NOS: 69  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 45  
LENGTH: 206  
TYPE: PRT  
ORGANISM: Homo Sapiens  
US-10-087-190-45

Query Match 99.0%; Score 1036.5; DB 4; Length 206;  
Best Local Similarity 99.5%; Pred. No. 3e-77;  
Matches 205; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MSKKKGSAEKKRTMMEIFSETKDVFLQKLEKAPKEKGTITMSVKEVLSLVDDGMV 60  
DB 1 MSKKKGSAEKKRTMMEIFSETKDVFLQKLEKAPKEKGTITMSVKEVLSLVDDGMV 60  
QY 61 DCEIGTSNYWAFPSKALHARKHKLTVLESQ-LSEGSQKASLOKSIIEKAKIGRCETEE 119  
DB 61 DCEIGTSNYWAFPSKALHARKHKLTVLESQ-LSEGSQKASLOKSIIEKAKIGRCETEE 120  
QY 120 RTRLAKELSLRDQREQLAEVKKYKDCDPQVEEIRQANKVAKAANRTDNI1PAIKSW 179  
DB 121 RTRLAKELSLRDQREQLAEVKKYKDCDPQVEEIRQANKVAKAANRTDNI1PAIKSW 180  
QY 180 AKRKGFEENKIDRTFGIPEDPDYID 205  
DB 181 AKRKGFEENKIDRTFGIPEDPDYID 206

RESULT 12  
US-10-087-190-24

Sequence 24, Application US/10087190  
Publication No. US20030223997A1  
GENERAL INFORMATION:

APPLICANT: Agensys, Inc.  
APPLICANT: Challita-Bid, Pia M.  
APPLICANT: Hubert, Rene S.  
APPLICANT: Raitano, Arthur B.  
APPLICANT: Farris, Mary  
APPLICANT: Afari, Daniel E. H.  
APPLICANT: Ge, Wangmao  
APPLICANT: Jakobovits, Aya  
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN  
TITLE OF INVENTION: ENTITLED 121P11 USERFUL IN TREATMENT AND DETECTION OF CANCER  
FILE REFERENCE: 51158-20034.20  
CURRENT APPLICATION NUMBER: US/10/087.190  
CURRENT FILING DATE: 2003-01-28  
PRIOR APPLICATION NUMBER: US 09/779,250  
PRIOR FILING DATE: 2001-03-05  
NUMBER OF SEQ ID NOS: 69  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 24  
LENGTH: 198  
TYPE: PRT  
ORGANISM: Homo Sapiens  
US-10-087-190-24

Query Match 96.6%; Score 1011; DB 4; Length 198;

Best Local Similarity 100.0%; Pred. No. 3.5e-75;  
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KGLSAEKKRTMMEIFSETKDVFLQKLEKAPKEKGTITMSVKEVLSLVDDGMVDCER 64  
DB 1 KGLSAEKKRTMMEIFSETKDVFLQKLEKAPKEKGTITMSVKEVLSLVDDGMVDCER 60  
QY 65 IGTSNYYWAFPSKALHARKHKLTVLESQ-LSEGSQKASLOKSIIEKAKIGRCETERTLA 124  
DB 61 IGTSNYYWAFPSKALHARKHKLTVLESQ-LSEGSQKASLOKSIIEKAKIGRCETERTLA 120  
QY 125 KELSRLDQREQLAEVKKYKDCDPQVEEIRQANKVAKAANRTDNI1PAIKSWAKRF 184  
DB 121 KELSRLDQREQLAEVKKYKDCDPQVEEIRQANKVAKAANRTDNI1PAIKSWAKRF 180  
QY 185 GFENKIDRTFGIPEDPD 202  
DB 181 GFENKIDRTFGIPEDPD 198

RESULT 13  
US-11-125-805-720

Sequence 720, Application US/11125805  
Publication No. US20050208039A1  
GENERAL INFORMATION:

APPLICANT: Pia M. Challita-Bid  
APPLICANT: Rene S. Hubert  
APPLICANT: Steve Chappell Mitchell  
APPLICANT: Arthur B. Raitano  
APPLICANT: Mary Farris  
APPLICANT: Daniel E.H. Afari  
APPLICANT: Aya Jakobovits  
TITLE OF INVENTION: 121P11: A TISSUE SPECIFIC PROTEIN  
TITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCERS  
FILE REFERENCE: 129.34US01 (511582003400)  
CURRENT FILING DATE: 2005-05-09  
PRIOR APPLICATION NUMBER: US/11/125.805  
PRIOR FILING DATE: 2003-07-14  
NUMBER OF SEQ ID NOS: 721  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 720  
LENGTH: 198  
TYPE: PRT  
ORGANISM: Schizosaccharomyces pombe  
US-11-125-805-720

Query Match 96.6%; Score 1011; DB 6; Length 198;  
Best Local Similarity 100.0%; Pred. No. 3.5e-75;  
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KGLSAEKKRTMMEIFSETKDVFLQKLEKAPKEKGTITMSVKEVLSLVDDGMVDCER 64  
DB 1 KGLSAEKKRTMMEIFSETKDVFLQKLEKAPKEKGTITMSVKEVLSLVDDGMVDCER 60  
QY 65 IGTSNYYWAFPSKALHARKHKLTVLESQ-LSEGSQKASLOKSIIEKAKIGRCETERTLA 124  
DB 61 IGTSNYYWAFPSKALHARKHKLTVLESQ-LSEGSQKASLOKSIIEKAKIGRCETERTLA 120  
QY 125 KELSRLDQREQLAEVKKYKDCDPQVEEIRQANKVAKAANRTDNI1PAIKSWAKRF 184  
DB 121 KELSRLDQREQLAEVKKYKDCDPQVEEIRQANKVAKAANRTDNI1PAIKSWAKRF 180  
QY 185 GFENKIDRTFGIPEDPD 202  
DB 181 GFENKIDRTFGIPEDPD 198

RESULT 14

US-10-087-190-13  
Sequence 13, Application US/10087190  
Publication No. US20030223997A1  
GENERAL INFORMATION:

\*APPLICANT: Agensys, Inc.  
; APPLICANT: Chailita-Bid, Pia M.  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Raltano, Arthur B.  
; APPLICANT: Faris, Mary  
; APPLICANT: Afar, Daniel E. H.  
; APPLICANT: Ge, Mangmao  
; APPLICANT: Jakobovitz, Aya  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN  
; FILE REFERENCE: 51158-20034.20  
; CURRENT FILING DATE: 2003-01-28  
; PRIOR FILING DATE: 2001-03-05  
; NUMBER OF SEQ ID NOS: 69  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 190  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-087-190-13

Query Match 93.1%; Score 975; DB 4; Length 190;  
Best Local Similarity 100.0%; Pred. No. 3e-72;  
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 16 MMEIFSETKQVFOQLKDEKIAPEKGIITAMSVKEVLQSLVDGAVDCERIGTSNYNAFP 75  
Db 1 MMEIFSETKQVFOQLKDEKIAPEKGIITAMSVKEVLQSLVDGAVDCERIGTSNYNAFP 60  
QY 76 SKALHARKHLEVLSEQLSEGSQKHALSLQKSIIEKAKIGRCETERTTLAKELSLRDRE 135  
Db 61 SKALHARKHLEVLSEQLSEGSQKHALSLQKSIIEKAKIGRCETERTTLAKELSLRDRE 120  
QY 136 QLKAEVEKYKDCDPQVVEIRQANKVAKAANRWTDNIFAIKSWAKKFGFEENKIDRTF 195  
Db 121 QLKAEVEKYKDCDPQVVEIRQANKVAKAANRWTDNIFAIKSWAKKFGFEENKIDRTF 180  
QY 196 GIPEDFDYID 205  
Db 181 GIPEDFDYID 190

RESULT 15  
US-10-087-190-19  
; Sequence 19, Application US/10087190  
; Publication NO. US2003022397A1  
; GENERAL INFORMATION:  
; APPLICANT: Agensys, Inc.  
; APPLICANT: Chailita-Bid, Pia M.  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Raltano, Arthur B.  
; APPLICANT: Faris, Mary  
; APPLICANT: Afar, Daniel E. H.  
; APPLICANT: Ge, Mangmao  
; APPLICANT: Jakobovitz, Aya  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN  
; FILE REFERENCE: 51158-20034.20  
; CURRENT FILING DATE: 2003-01-28  
; PRIOR FILING DATE: 2001-03-05  
; NUMBER OF SEQ ID NOS: 69  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 190  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-087-190-19

Query Match 93.1%; Score 975; DB 4; Length 190;

Best Local Similarity 100.0%; Pred. No. 3e-72;  
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 16 MMEIFSETKQVFOQLKDEKIAPEKGIITAMSVKEVLQSLVDGAVDCERIGTSNYNAFP 75  
Db 1 MMEIFSETKQVFOQLKDEKIAPEKGIITAMSVKEVLQSLVDGAVDCERIGTSNYNAFP 60  
QY 76 SKALHARKHLEVLSEQLSEGSQKHALSLQKSIIEKAKIGRCETERTTLAKELSLRDRE 135  
Db 61 SKALHARKHLEVLSEQLSEGSQKHALSLQKSIIEKAKIGRCETERTTLAKELSLRDRE 120  
QY 136 QLKAEVEKYKDCDPQVVEIRQANKVAKAANRWTDNIFAIKSWAKKFGFEENKIDRTF 195  
Db 121 QLKAEVEKYKDCDPQVVEIRQANKVAKAANRWTDNIFAIKSWAKKFGFEENKIDRTF 180  
QY 196 GIPEDFDYID 205  
Db 181 GIPEDFDYID 190

Search completed: February 2, 2006, 12:56:14  
Job time : 173 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 2, 2006, 12:53:27 ; Search time 8 Seconds

(without alignments)  
300.275 Million cell updates/sec

Title: US-10-087-190-3

Perfect score: 1047

Sequence: 1 MSKKKGSAEKRTRMEIF.....FEENKIDRTFGIPEDFDYID 205

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 88029 seqs, 11718060 residues

Total number of hits satisfying chosen parameters: 88029

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA New:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEM\_PUB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEM\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEM\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US09\_NEM\_PUB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10\_NEM\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_NEM\_PUB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US12\_NEM\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEM\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	117	11.2	976	US-11-155-288-20	Sequence 20, Appl
2	108.5	10.4	860	US-11-019-711-59	Sequence 59, Appl
3	106	10.1	1786	US-11-196-400-3	Sequence 3, Appl
4	100.5	9.6	1976	US-11-069-834-52	Sequence 52, Appl
5	100.5	9.6	2665	US-11-124-368A-214	Sequence 214, App
6	98	9.4	2668	US-11-124-368A-215	Sequence 215, App
7	97.5	9.3	1976	US-11-069-834-54	Sequence 54, App
8	96	9.2	171	US-10-821-234-994	Sequence 994, App
9	95.5	9.1	1960	US-11-069-834-48	Sequence 48, Appl
10	94	9.0	284	US-10-821-234-1532	Sequence 1632, Ap
11	93	8.9	248	US-10-878-556A-175	Sequence 175, Appl
12	91.5	8.7	1992	US-11-069-834-58	Sequence 58, Appl
13	91.5	8.7	2000	US-11-069-834-56	Sequence 56, Appl
14	91.5	8.7	664	US-10-878-556A-44	Sequence 44, Appl
15	91	8.7	1995	US-11-069-834-60	Sequence 60, Appl
16	91	8.7	2261	US-10-995-561-600	Sequence 600, App
17	91	8.7	2261	US-10-511-545-1	Sequence 1, Appl
18	91	8.7	2261	US-10-055-309A-9	Sequence 9, Appl
19	91	8.7	2261	US-11-055-309A-10	Sequence 10, Appl
20	90.5	8.6	1960	US-10-857-780-23	Sequence 23, Appl
21	90.5	8.6	2101	US-10-857-780-23	Sequence 23, Appl
22	90	8.6	776	US-10-821-234-1171	Sequence 1171, Ap
23	89.5	8.5	1388	US-10-821-234-1143	Sequence 1143, Ap
24	89.5	8.5	1410	US-10-878-556A-136	Sequence 136, App
25	89.5	8.5	1586	US-10-821-234-901	Sequence 901, App

26	88.5	8.5	1404	US-10-878-556A-169	Sequence 169, App
27	88	8.4	1299	US-10-821-234-1145	Sequence 1145, Ap
28	88	8.4	3803	US-10-995-561-773	Sequence 773, App
29	88	8.4	3960	US-10-995-561-771	Sequence 771, App
30	88	8.4	5335	US-10-995-561-777	Sequence 777, App
31	88	8.4	5406	US-10-995-561-774	Sequence 774, App
32	88	8.4	5415	US-10-995-561-779	Sequence 779, App
33	88	8.4	5464	US-10-995-561-775	Sequence 775, App
34	87.5	8.4	1732	US-10-055-877-147	Sequence 147, App
35	86	8.2	1663	US-10-055-877-148	Sequence 148, App
36	85	8.1	227	US-11-215-658-12	Sequence 12, Appl
37	85	8.1	693	US-10-873-626-185	Sequence 185, App
38	84.5	8.1	448	US-10-793-626-1728	Sequence 1728, Ap
39	84.5	8.1	1641	US-10-877-346-40	Sequence 40, Appl
40	84.5	8.1	2107	US-10-995-561-827	Sequence 827, App
41	84.5	8.1	2480	US-10-995-561-825	Sequence 825, App
42	84.5	8.1	3116	US-10-995-561-826	Sequence 826, App
43	84	8.0	663	US-11-196-475-70	Sequence 70, Appl
44	84	8.0	663	US-11-196-475-78	Sequence 78, Appl
45	84	8.0	1652	US-10-995-561-663	Sequence 663, App

## ALIGNMENTS

RESULT 1  
US-11-155-288-20  
; Sequence 20, Application US/11155288  
; Publication NO. US20060008468A1  
; GENERAL INFORMATION:  
; APPLICANT: Chiang, Chih-Sheng  
; APPLICANT: Simard, John J.L.  
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED  
; FILE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS  
; CURRENT FILING DATE: 2005-06-17  
; PRIOR APPLICATION NUMBER: 60/580,969  
; PRIOR FILING DATE: 2004-06-17  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 976  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-155-288-20

Query Match 11.2% Score 117; DB 7; Length 976;  
Best Local Similarity 23.9% Pred. No. 0.094;  
Matches 63; Conservative 38; Mismatches 85; Indels 78; Gaps 13;

3 KKKGISAE--KRTMEL-PSYEDV-----FOLKDEKIPKKEGIRAMSVKEVL 51  
413 QKSSLEBEMTKLTNNKEVELEKKGVEKETTLLYENKQFKIABELKG-TEOBELIGLL 471  
52 OSL---VDDGWDCRIGTSNYTAPPSKAL-----HARKHLEVLK-- 90  
472 QAREKVEHDLIQLTRITTSBOYKSEYKDLTELENKTLKNTBELTSHONKSLKNEKLT 531  
91 -----SOLSEGSQKHAISLOKSIKAKIGACETEERTRLAKESLSLDQREQ 136  
532 QETSDMTLEKNQGDINNKKQKQEBRLKQIE--NLQETETQLRNELEFVREBKQKQKDE 589  
137 LKAEVEKYD-CD-----PQVEEIRQANKYAKK--ANRRTDNIFAK----- 177  
530 VKCKDKSEBENCNLRKOVENKRYIEBLQDENKALKKKGTAESKQNLVYEIKVKNLELE 649  
QY 178 -SWAKKFG-----FEENKI 191  
DB 650 LSAKQKFGELITDTYQKIEBDKTI 673

RESULT 2



```
US-11-019-711-59
; Sequence 59, Application US/11019711
; Publication No. US2006009634A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsebrook II, John P
; APPLICANT: Tchenev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Paturajan, Meera
; APPLICANT: Grose, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyanek, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigara, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Eisen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/11/019,711
; PRIOR FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US/10/037,417
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 860
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Myosin Tail
; OTHER INFORMATION: Consensus Sequence
US-11-019-711-59

Query Match          10.4%; Score 108.5; DB 7; Length 860;
Best Local Similarity 28.1%; Pred. No. 0.36;
Matches 43; Conservative 27; Mismatches 58; Indels 25; Gaps 6;

QY 13 RTRMEISRTDVQDLKELKARKGKITMSYKVEYQSLVYDGMDCERIGSNYYW 72
DB 126 RKKQDAINEISE--QISOLQKQAK-----AEKESQQLQAEVDLLAQDLDSI----- 171
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QY 73 AFPSKA-LHARKKLEVLSEQLSEGSQKHSLOKSIKAKIGRCETERTRLAKELSLR 131
DB 172 ---TKAKINAEK-KAKQLESQSLQYKLDLQRLQDL-----TSQKSLQSENSDLT 221
QY 132 DQESQLAEVEKYDCDQPVVEIRQANKVAK 164
DB 222 RQLEAEHQVSNLSKLSQLESQLEAKRSISE 254

RESULT 3
US-11-196-400-3
; Sequence 3, Application US/11196400
; Publication No. US20050287166A1
; GENERAL INFORMATION:
; APPLICANT: DRUTHE, PIERRE
; APPLICANT: DAUBERSIES, PIERRE
; TITLE OF INVENTION: MALALIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
; FILE REFERENCE: 200773USODIV
; CURRENT APPLICATION NUMBER: US/11/196,400
; PRIOR FILING DATE: 2005-08-04
; PRIOR APPLICATION NUMBER: US/09/742,096
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 08/973,462
; PRIOR FILING DATE: 1998-02-06
; PRIOR APPLICATION NUMBER: PCT/FR96/00894
; PRIOR FILING DATE: 1996-06-12
; PRIOR APPLICATION NUMBER: FR 95/07007
; PRIOR FILING DATE: 1995-06-13
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: P. falciparum
US-11-196-400-3

Query Match          10.1%; Score 106; DB 7; Length 1786;
Best Local Similarity 18.7%; Pred. No. 1.3;
Matches 47; Conservative 55; Mismatches 77; Indels 72; Gaps 9;

QY 2 SKKKGLSAEKRRTMMEIFSETKD-----VFQDLKELKPKKGTMTAMSVKYLQ 52
DB 1186 SKERTESIKDKKQVSLVEEVQDMDSEVKYELKMEBELMKD---AVEINDITS 1241
QY 53 SLVVD---GMVDCERIGTSNYWAFPSKALHARKKLEVLSEQLSEGSQ-----KHSLS 103
DB 1242 KLIEBTQELNEVADLI-----KOMERKLEIKELKSLSDSKETIIDAKDPTL 1286
QY 104 QKSIKKA-----KIGRCETERTRLAKELSLRDQRLQKAEVEKYKCDQPVVEIR 155
DB 1287 EKVIEEHDITTTLDDEVVELKDVEEDKLEK-VSDLKDLBIDLKVEKEIKELSESILBDY 1345
QY 156 RQANKV-----AKEAARNWTNIPAIKSMARKKGFGEENKIDR 193
DB 1346 KELKTITETDILKEKKKIEKDHFKFEEBAEBSIKDLBIDLKVESSLVE---EKKKLE 1401
QY 194 TFGIPEDFDYI 204
DB 1402 VHELKEVEYEH 1412

RESULT 4
US-11-069-834-52
; Sequence 52, Application US/11069834
; Publication No. US20050276811A1
; GENERAL INFORMATION:
; APPLICANT: CARROLL, MICHAEL C.
; APPLICANT: MOORE JR., FRANCIS D.
; APPLICANT: HECHTMAN, HERBERT B.
; TITLE OF INVENTION: NATURAL IGM ANTIBODIES AND INHIBITORS THEREOF
; FILE REFERENCE: CRA-002.01
; CURRENT APPLICATION NUMBER: US/11/069,834
; CURRENT FILING DATE: 2005-03-01
```

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;; PRIOR APPLICATION NUMBER: 60/588,648
;; PRIOR FILING DATE: 2004-07-16
;; PRIOR APPLICATION NUMBER: 60/549,123
;; PRIOR FILING DATE: 2004-03-01
;; NUMBER OF SEQ ID NOS: 65
;; SOFTWARE: PatentIn Ver. 3.3
;; SEQ ID NO: 52
;; LENGTH: 1976
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-11-069-834-52

Query Match          9.6%; Score 100.5; DB 7; Length 1976;
Best Local Similarity 24.7%; Pred. No. 4;
Matches 49; Conservative 40; Mismatches 50; Indels 59; Gaps 9;

QY 10 EKKTRMEIFSETGV-FOLKDEKIAPKKKG-----ITMS-----VKFVL--- 51
DB 934 EEBRQIIQ--NEKKQMAHIODLEEQDEEGANQKIQLEKVTIAKIKKMEEVLLLE 991
QY 52 -----QSLVDDGAVDCERIGTSNYWAFPSKALHARK--HKLLEYLSQSGSKH 100
DB 992 DQNSKFIKKKLMEDRIAC-----SSQLAEERKAKYLAKIRNKQVWISDLBERLKE 1046
QY 101 ASLQSKIKAKIGRCETERTRLAKELSLRDQEQLAQVEKYQCDPQVEEIR--- 156
DB 1047 EKTROELEKAK-----RKLDEETJLDQIQIAEQVDELKVQTLKKEEELQCALA 1097
QY 157 -----QANKYAKE 164
DB 1098 RGDEETLHKNNALKVARE 1115

RESULT 5
US-11-124-368A-214
; Sequence 214, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
; FILE REFERENCE: CLO01524
; CURRENT APPLICATION NUMBER: US/11/124,368A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/625,936
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 214
; LENGTH: 2665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-368A-214

Query Match          9.6%; Score 100.5; DB 7; Length 2665;
Best Local Similarity 20.3%; Pred. No. 5.7;
Matches 41; Conservative 49; Mismatches 71; Indels 41; Gaps 7;

QY 1 MSKKKGLSAEKR--TRMEIFSETGVFOLKDEKIAPKKGIYAMSVKVELQSLVDD-- 56
DB 1737 IDKLRGIVSEKTNESNNQKLEHSDALKKQDILK--IOEIRIRAHMHLKE--QOETIDKL 1793
QY 57 -----DGAVDCER-IGTSNYWAFPSKALHARKHKLLEYLSQSGSKHSLQSKI 107
DB 1794 RGIYSEKTDKLSNNQKLEHSDALKKQDILK--IOEIRIRAHMHLKE--QOETIDKL 1853
QY 108 EKAK-----IGRCETE-----ERTRLAKELSLRDQEQLAQVE 142
DB 1854 KQIKDQSLTSLKLEINLNAQKLEHSDALKKQDILK--IOEIRIRAHMHLKE--QOETIDKL 1913
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QY 143 KYKCDPQVEEIRQANKYAKE 164
DB 1914 ETKARDLEIQOELKTARMLSKKE 1935

RESULT 6
US-11-124-368A-215
; Sequence 215, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
; FILE REFERENCE: CLO01524
; CURRENT APPLICATION NUMBER: US/11/124,368A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/625,936
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 215
; LENGTH: 2668
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-368A-215

Query Match          9.4%; Score 98; DB 7; Length 2668;
Best Local Similarity 20.7%; Pred. No. 8.8;
Matches 42; Conservative 47; Mismatches 72; Indels 42; Gaps 7;

QY 1 MSKKKGLSAEKR--TRMEIFSETGVFOLKDEKIAPKKGIYAMSVKVELQSLVDD-- 57
DB 1740 IDKLRGIVSEKTNESNNQKLEHSDALKKQDILK--IOEIRIRAHMHLKE--QOETIDKL 1796
QY 58 -GAVDCERIGTSNYWAFPS-----KALHARKHKLLEYLSQSGSKHSLQSKS 106
DB 1797 RGIYSEKTDKLSNNQKLEHSDALKKQDILK--IOEIRIRAHMHLKE--QOETIDKL 1856
QY 107 IEKAK-----IGRCETE-----ERTRLAKELSLRDQEQLAQVE 141
DB 1857 KQIKDQSLTSLKLEINLNAQKLEHSDALKKQDILK--IOEIRIRAHMHLKE--QOETIDKL 1916
QY 142 EKYKCDPQVEEIRQANKYAKE 164
DB 1917 QETKARDLEIQOELKTARMLSKKE 1939

RESULT 7
US-11-069-834-54
; Sequence 54, Application US/11069834
; Publication No. US20050276811A1
; GENERAL INFORMATION:
; APPLICANT: CARROLL, MICHAEL C.
; APPLICANT: MOORE JR., FRANCIS D.
; APPLICANT: HECHTMAN, HERBERT B.
; TITLE OF INVENTION: NATURAL IGM ANTIBODIES AND INHIBITORS THEREOF
; FILE REFERENCE: CRA-002.01
; CURRENT APPLICATION NUMBER: US/11/069,834
; CURRENT FILING DATE: 2005-03-01
; PRIOR APPLICATION NUMBER: 60/588,648
; PRIOR FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: 60/549,123
; PRIOR FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO: 54
; LENGTH: 1976
; TYPE: PRT
```

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; ORGANISM: Homo sapiens
US-11-069-834-54

Query Match
Best Local Similarity 23.6%; Score 97.5; DB 7; Length 1976;
Matches 41; Conservative 37; Mismatches 61; Indels 35; Gaps 7;

Cy 1 MSKKGLSAEKRTRMEIFSETKDVFLQKLE-KIAPEKGTITMSYKVELQSLVDDGM 59
Db 878 MERGHQOULEKKNILAEQLQAEITLFAEAEEMRAIALAKQ-----ELERIHDLSEKVE 932

Cy 60 VDCERIGTSNYWYAFPSKALHARKHKLKV-----LESQI--SGSOKHASLQKSTIEKATIG 113
Db 933 EEBER-----NQLQNEKKKQWQAHYQDLSEQLDEBEGAKQKQLERKVTAEAKIK 981

Cy 114 RCETEERTLAKELSLDQR-----EQLKAEVEKYKCDPQVEEIRQANVAK 163
Db 982 KME-----EELILLEDQNSKPIKKEKKLMEDRIABESQSLAEERAKNVLAK 1027

RESULT 8
US-10-821-234-994
; Sequence 994, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andamanl, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 994
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-994

Query Match
Best Local Similarity 20.7%; Score 96; DB 6; Length 171;
Matches 36; Conservative 38; Mismatches 48; Indels 52; Gaps 6;

Cy 19 IFSETKDVFLQKLEKIA-----PKKGTITMSYKVELQSL 54
Db 20 LFTWASSDIQVLEKRAAGQAFELILSPRSKESVPEFPLSPPKKQDLSEIQKLEAA 79

Cy 55 VDDGVNDERIGTSNYWYAFPSKALHARKHKLKVLEVSQSLSEGSOKHASLQKSTIEKATIGR 114
Db 80 EE-----RRKSHAEVLYKQIAEKREKEVEYLQKAIENNNPS 116

Cy 115 CETERTRIAKELSLDQR-QLKAEVEKYKCDPQVEEIRQANVAKAAN 167
Db 117 KMAEE--KLTHKMEANKENREQAQMAKLERLREKQKH-IEEVRK-NKESKQPAD 166

RESULT 9
US-11-069-834-48
; Sequence 48, Application US/11069834
; Publication No. US20050276811A1
; GENERAL INFORMATION:
; APPLICANT: CARROLL, MICHAEL C.
; APPLICANT: MOORE JR., FRANCIS D.
; APPLICANT: HECHTMAN, HERBERT B.
; TITLE OF INVENTION: NATURAL IGM ANTIBODIES AND INHIBITORS THEREOF
; FILE REFERENCE: CRA-002.01
; CURRENT APPLICATION NUMBER: US/11/069,834
; CURRENT FILING DATE: 2005-03-01
; PRIOR APPLICATION NUMBER: 60/588,648
```

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; PRIOR FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: 60/549,123
; PRIOR FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 48
; LENGTH: 1960
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-069-834-48

Query Match
Best Local Similarity 24.1%; Score 95.5; DB 7; Length 1960;
Matches 51; Conservative 37; Mismatches 65; Indels 59; Gaps 9;

Cy 8 SAEKRTRMEIFSETKDVFLQKLEKIAPEKGTITAM-----SVKEVQLSLVDDGMVDC 62
Db 1382 TAEAKRQLQ-----KOLEGLSQLEKVAAYDLEKTKRTLQQLDELDDLVLVDL 1429

Cy 63 --ERIGTSNYWYAFPSKALHARKHKLKV-----ESQISEGSOKHAS 102
Db 1430 DHQKQSVN-----LEKKQKFFQLAEKRTISAKVAERDRAEAREKRTKALS 1480

Cy 103 LQKSI-----KAKIGCETERTRIAKELSLDQRQOLKAEVEKYKCDPQVEEIR- 156
Db 1481 LARLEAMEQKALERLNKQFRTWM-EDLWSSKDVGKSVHELEKSRALAEQVEEEMKT 1539

Cy 157 -----QANKVAKAANRWTDNIFAISWAKR 182
Db 1540 QLEELDELDQATEDAKRLKLVNQLQAKAQFER 1571
```

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RESULT 10
US-10-821-234-1632
; Sequence 1632, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andamanl, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 1632
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1632

Query Match
Best Local Similarity 9.0%; Score 94; DB 6; Length 284;
Matches 51; Conservative 30; Mismatches 73; Indels 54; Gaps 8;

Cy 2 SKKGLSAEKRTRMEIFSETKDVFLQKLEKIAPEKGTITMSYKVELQSLVDD----G 58
Db 67 AQEKLEQAEKATDAEDVASLNRRIQLVEBELDRAOERLTLQKLEBAKADESERG 126

Cy 59 MVDCERIGTSNYWYAFPSKALHAR-----KHLLEVLSQSLSEGSOKH----- 100
Db 127 W-----KVIENDAMKDEEKKEILOEMQLKKA--KHLAEDSDRKYEVAR 167

Cy 101 -----ASLQKSTIEKAKIGCETERTRIAKELSLDQRQOLKAEVEKYKCDPQVE 153
Db 168 KLIVILEGLSESRARV-----ASPRARQLDEELRTMQALKSLSMASEEVSTEDKYE 223

Cy 154 EIRQANKVAKAANRWTDNIFAISWAK 181
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Job time : 9 secs

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 664
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER:
; DATABASE ENTRY DATE: 1986-07-21
US-10-878-556A-44

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Query Match      8.7%; Score 91; DB 6; Length 664;
Best Local Similarity 24.5%; Pred. No. 5.9;
Matches 45; Conservative 24; Mismatches 55; Indels 60; Gaps 9;

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QY      8 SAEEKRTMMEIFSETKDVF-----QLKDLKIA-PKEKGI-TAMS 46
      94 SVAKERARLQLELSVYREEFKELKARNYKESGDLIAQARLKDLKALNSKEALSTALS 153
      47 VKEVQLSDVD--GMYD-----CERIGTSNYWAFPSKALHARKKLE 87
      154 EKRTLEGELHDLRGQVAKLEBALGRKKQLQDEMLRVDAN-----RLQTKKEILD 205
QY      88 -----VLSEQLSGSQKHSLOKSIKAKIGRCETERTRIAKELSLR----DORSEOLKA 139
      206 FQKNYISEELRETKRHETRLVEINDGK---QREFESRLADALQELRAQHEDEVQYTK 261
      140 EVER 143
      262 ELER 265
      262 ELER 265

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RESULT 15
US-11-069-834-60
; Sequence 60, Application US/11069834
; Publication No. US20050276811A1
; GENERAL INFORMATION:
; APPLICANT: CARROLL, MICHAEL C.
; APPLICANT: MOORE JR., FRANCIS D.
; APPLICANT: HECHTMAN, HERBERT B.
; TITLE OF INVENTION: NATURAL IGM ANTIBODIES AND INHIBITORS THEREOF
; FILE REFERENCE: CRA-002.01
; CURRENT APPLICATION NUMBER: US/11/069,834
; CURRENT FILING DATE: 2005-03-01
; PRIOR APPLICATION NUMBER: 60/588,648
; PRIOR FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: 60/549,123
; PRIOR FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 60
; LENGTH: 1995
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-069-834-60

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Query Match      8.7%; Score 91; DB 7; Length 1995;
Best Local Similarity 23.9%; Pred. No. 22;
Matches 43; Conservative 33; Mismatches 50; Indels 54; Gaps 8;

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QY      8 SAEEKRTMMEIFSETKDVFQKLEKTAPEKKGITAMSVKEVQLSDVDGKMDCCER--- 64
      1414 AARAEALTORLAETKTEVDRL-----ERG-----RRRLQOEIDDMTDLQORQ 1458
QY      65 -IGTSNYWAFPSKALHARKKLEVLSEQLSGSQKHSLOKSIKAKIGRCETERTRL 123
      1459 LVST-----LEKKQKFPDQL-----AEKKAALVAVERE--RAEAERERE 1499
QY      124 AKELSL-----SLRDQREQLKAEVE---KYDCDPQVVEEIRQANKVAKAEAN 167
      1500 ABALSLTALBEEQAREELERQNRALRALLEALLSSKDDVGKSVHELERACRAVAEQAN 1559

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Search completed: February 2, 2006, 12:56:28